

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2003, 17:59:09 ; Search time 64 Seconds
(without alignments)
281.337 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATROGKPSNLRARCSR.....ANNVVKQEDVYVSCGR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	645	99.4	119	8 US-08-945-459A-1	Sequence 1, Appli
2	645	99.4	119	10 US-09-068-253-2	Sequence 2, Appli
3	645	99.4	120	10 US-09-945-182-4	Sequence 4, Appli
4	645	99.4	501	8 US-08-981-490B-1	Sequence 1, Appli
5	640	98.6	119	10 US-09-880-708-13	Sequence 13, Appl
6	640	98.6	495	10 US-09-880-708-10	Sequence 10, Appl
7	639	98.5	502	10 US-09-813-398-37	Sequence 37, Appl
8	629	96.9	501	9 US-09-730-772-13	Sequence 13, Appl
9	629	96.9	501	9 US-09-735-849-13	Sequence 13, Appl
10	629	96.9	501	12 US-10-379-830-13	Sequence 13, Appl
11	540	83.2	321	10 US-09-945-182-26	Sequence 26, Appl
12	538	82.9	263	10 US-09-945-182-32	Sequence 32, Appl
13	528	81.4	436	9 US-09-730-772-14	Sequence 14, Appl
14	528	81.4	436	9 US-09-735-849-14	Sequence 14, Appl
15	528	81.4	436	12 US-10-379-830-14	Sequence 14, Appl

16	494	76.1	294	10	US-09-945-182-2	Sequence 2, Appli
17	494	76.1	388	10	US-09-945-182-34	Sequence 34, Appl
18	494	76.1	411	10	US-09-945-182-28	Sequence 28, Appl
19	494	76.1	450	15	US-10-188-246-12	Sequence 12, Appl
20	489	75.3	240	10	US-09-945-182-30	Sequence 30, Appl
21	385	59.3	72	10	US-09-945-182-15	Sequence 15, Appl
22	348	53.6	72	10	US-09-945-182-13	Sequence 13, Appl
23	347	53.5	117	14	US-10-115-406-13	Sequence 13, Appl
24	347	53.5	117	15	US-10-154-333-15	Sequence 15, Appl
25	347	53.5	118	10	US-09-813-459-10	Sequence 10, Appl
26	347	53.5	118	10	US-09-859-211-37	Sequence 37, Appl
27	347	53.5	118	10	US-09-880-708-15	Sequence 15, Appl
28	347	53.5	118	11	US-09-872-856-37	Sequence 37, Appl
29	347	53.5	118	15	US-10-335-483-19	Sequence 19, Appl
30	347	53.5	129	11	US-09-804-625-5	Sequence 2, Appli
31	347	53.5	143	14	US-10-002-278-3	Sequence 3, Appli
32	347	53.5	396	8	US-08-957-425-5	Sequence 5, Appli
33	347	53.5	396	9	US-09-952-360-2	Sequence 2, Appli
34	347	53.5	396	11	US-09-804-625-4	Sequence 4, Appli
35	347	53.5	396	12	US-10-139-814-2	Sequence 2, Appli
36	347	53.5	396	12	US-10-236-152A-2	Sequence 2, Appli
37	347	53.5	396	12	US-10-210-951-46	Sequence 46, Appl
38	347	53.5	396	12	US-10-211-884-46	Sequence 46, Appl
39	347	53.5	396	12	US-10-346-723-2	Sequence 2, Appli
40	347	53.5	396	14	US-10-044-716-2	Sequence 2, Appli
41	347	53.5	396	15	US-10-122-026-10	Sequence 0, Appli
42	347	53.5	397	10	US-09-813-398-24	Sequence 24, Appl
43	344	53.0	118	14	US-10-115-406-15	Sequence 15, Appl
44	344	53.0	118	15	US-10-154-333-17	Sequence 17, Appl
45	344	53.0	143	14	US-10-002-278-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-945-459A-1
; Sequence 1, Application US/08945459A
; Publication No. US20020102633A1
; GENERAL INFORMATION:
; APPLICANT: MAKISHINA, FUSAO; TAKAMATSU,
; APPLICANT: HIROYUKI; MIKI, HIDEO; KAWAI,
; APPLICANT: SHINJI; KIMURA, MICHIO; MATSUMOTO,
; APPLICANT: TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
; APPLICANT: KOICHI; SATOH, YUSUKE
; TITLE OF INVENTION: A NOVEL PROTEIN AND
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCE: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
; ADDRESSER: LLP
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,459A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/01062
; FILING DATE: 19-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP7/322403
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP7/93664
; FILING DATE: 19-APR-1995

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ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
US-08-945-459A-1
Query Match 99.4%; Score 645; DB 8; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.3e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
DB 1 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 119
DB 61 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 119
RESULT 2
US-09-068-253-2
Sequence 2, Application US/09068253
Patent No. US2002016381A1
GENERAL INFORMATION:
APPLICANT: SHIMURA, Takesada
TITLE OF INVENTION: TORIYAMA, Satoshi
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146.1286
CURRENT APPLICATION NUMBER: US/09/068,253
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/JP96/03333
PRIOR FILING DATE: 1996-11-14
PRIOR APPLICATION NUMBER: JP 7/322402
PRIOR FILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-253-2
Query Match 99.4%; Score 645; DB 10; Length 119;
Best Local Similarity 99.2%; Pred. No. 1.3e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 119
DB 61 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 119
RESULT 3
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US-09-945-182-4
Sequence 4, Application US/09945182
Patent No. US2002016049A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
Wozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
STATE: Massachusetts
COUNTRY: USA
CITY: Cambridge
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-945-182-4
Query Match 99.4%; Score 645; DB 10; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.3e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 2 PLATROGKRPSKNLKARCSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 61
QY 61 PTNHAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 119
DB 62 PTNHAVIQTLNMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMNVESCGCR 120
RESULT 4
US-08-981-490B-1
Sequence 1, Application US/08981490B
Publication No. US20020045568A1
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulista, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF T
TITLE OF INVENTION: NERVOUS SYSTEM
FILE REFERENCE: 100564-07032
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; CURRENT APPLICATION NUMBER: US/08/981,490B
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match          99.4%; Score 645; DB 8; Length 501;
Best Local Similarity 99.2%; Pred. No. 6.4e-62;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 383 PLATGKGRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSHLE 442

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DB 443 PTNHAIVIOTLANSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 5
US-09-880-708-13
; Sequence 13, Application US/09880708
; Patent No. US20020165361A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 619/677-1465
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13
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Query Match          98.6%; Score 640; DB 10; Length 119;
Best Local Similarity 98.3%; Pred. No. 4.4e-62;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 PLANRQGRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSHLE 60

QY 61 PTNHAIVIOTLANSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 61 PTNHAIVIOTLANSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

RESULT 6
US-09-880-708-10
; Sequence 10, Application US/09880708
; Patent No. US20020165361A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/003,144
; FILING DATE: 12-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 619/677-1465
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-880-708-10

Query Match          98.6%; Score 640; DB 10; Length 495;
Best Local Similarity 98.3%; Pred. No. 2.2e-61;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 377 PLANRQGRPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSHLE 436

QY 61 PTNHAIVIOTLANSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 437 PTNHAIVIOTLANSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 495
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RESULT 9
US-09-735-849-13
; Sequence 13, Application US/09735849
; Patent No. US20010037017A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Jr., Malcolm
; APPLICANT: Chang, Steven Chao-Huan
; TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
; PROTEINS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Fastseq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/735,849
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,081
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfeld, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/POCKET NUMBER: NIH099.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-735-849-13
Query Match 96.9%; Score 629; DB 9;
Best Local Similarity 97.5%; Pred. No. 3.5e-60;

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-730-772-14

Query Match 81.4%; Score 528; DB 9; Length 436;
Best Local Similarity 76.9%; Pred. No. 3e-49;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATROGKEPSKNLKARCSBKALHVNFRDMGDDWIIAPLEYEAFHCEGLCEFPPLRSHLEPT 62
Db 320 ASRRGKHGKKSLRCSKKPLHVNFKELGMDWIIAPLEYEAFHCEGVCDFPLRSHLEPT 379

QY 63 NHAIVQITLMSMDPSTPTACTPRLSTISILIFDLSANNVVVYQYEDMVMVESCGR 119
Db 380 NHAIVQITLMSMDPSTPTSCVPTKLTPTSLIYIDAGNNVYNEYEMVVMVESCGR 436

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RESULT 14
US-09-735-840-14
; Sequence 14, Application US/09735849
; Patent NO. US20010037017A1
; GENERAL INFORMATION:
; APPLICANT: Layten, Frank P.
; APPLICANT: Moos, Jr., Malcolm
; APPLICANT: Chang, Steven Chao-Huan
; TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

ADDRESS: Knudsen, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fastseq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/7735.849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001AFC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550

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; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-735-849-14

Query Match      81.4%; Score 528; DB 9; Length 436;
Best Local Similarity 76.9%; Pred. No. 3e-49;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATROGKRPSKNLKARCSRKALHVNFKDMGWDWIITAPLEYEAFHCEGLCEFPRLRSLEPT 62
Db 320 ASRHGRHGKSKRLRCCKPLHVNFKELGWDWIITAPLEYEAFHCEGLCEFPRLRSLEPT 379
QY 63 NHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
Db 380 NHAIQTLMNSMDPGSTPPSCVPTKLTPTISILYIDAGNNVYNEYEMVVEVESCGR 436

Search completed: September 26, 2003, 18:09:07
Job time : 71 secs

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RESULT 15
US-10-379-830-14
; Sequence 14, Application US/10379830
; Publication No. US20030176683A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; Moos, Jr., Malcolm
; Chang, Steven Chao-Huan
; TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
; PROTEINS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/379,830
; FILING DATE: 03-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,772
; FILING DATE: 30-NOV-2000
; APPLICATION NUMBER: 08/836,081
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfeld, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/DOCKET NUMBER: NIH099.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-379-830-14

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	645	99.4	501	1	GDF5_HUMAN	P43026 homo sapien
2	640	98.6	495	1	GDF5_MOUSE	P43027 mus musculus
3	543	83.7	125	1	GDF6_MOUSE	P43028 mus musculus
4	528	81.4	436	1	GDF6_BOVIN	P55106 bos taurus
5	493	76.0	151	1	GDF7_MOUSE	P43029 mus musculus
6	353.5	54.5	461	1	DVRL_STRPU	P48970 strongyloce
7	352	54.2	395	1	UNIV_STRPU	P48970 strongyloce
8	347	53.5	393	1	BMP2_RAT	P49001 rattus norv
9	347	53.5	394	1	BMP2_MOUSE	P21274 mus musculus
10	347	53.5	395	1	BMP2_RABIT	O46564 cryctolagus
11	347	53.5	396	1	BMP2_DAMDA	O19006 dama dama (
12	347	53.5	396	1	BMP2_HUMAN	P12643 homo sapien
13	347	53.5	401	1	BMP4_XENLA	P30895 xenopus lae
14	347	53.5	593	1	DECA_DROSTI	O17076 drosophila
15	346	53.3	405	1	BMP4_CHICK	O90752 gallus gall
16	344	53.0	588	1	DECA_DROME	P07713 drosophila
17	343	52.9	398	1	BMP4_XENLA	P25703 xenopus lae
18	343	52.9	398	1	BMP4_XENLA	P30894 xenopus lae
19	341	52.5	408	1	BMP4_MOUSE	P12175 mus musculus
20	341	52.5	408	1	BMP4_RAT	O06826 rattus norv
21	339	52.2	408	1	BMP4_HUMAN	P12644 homo sapien
22	338	52.1	372	1	DECA_TRICA	O26974 tribolium c
23	338	52.1	408	1	BMP4_DAMDA	O29607 dama dama (
24	337	51.9	353	1	BMP2_CHICK	O90751 gallus gall
25	336	51.8	409	1	BMP4_RABIT	O46576 cryctolagus
26	335	51.6	355	1	DVRL_STRPU	P35621 brachydanio
27	334	51.5	621	1	DECA_DROPS	P11699 drosophila
28	333	51.3	207	1	BMP6_RAT	O04906 rattus norv
29	333	51.3	452	1	BMP5_MOUSE	P49003 mus musculus
30	333	51.3	454	1	BMP5_HUMAN	P22003 homo sapien
31	332	51.2	513	1	BMP6_HUMAN	P22004 homo sapien
32	330	50.8	431	1	BMP7_HUMAN	P18075 homo sapien
33	329	50.7	510	1	BMP6_MOUSE	P20722 mus musculus

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [4];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -|- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -|- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -|- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
 CC HUMAN EMBRYONIC DEVELOPMENT.
 CC -|- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC
 CC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
 CC DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
 CC RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
 CC METACARPALS, METATARSALS AND PHALANGES ARE PARTICULARLY SHORT. THE
 CC PHALANGES ARE ALMOST SQUARE.
 CC -|- SIMILARITY: Belongs to the TGF-beta family.
 CC
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 CC
 CC EMBL; X80915; CAA56874.1; -;
 CC EMBL; U13660; AAX57007.1; -;
 CC EMBL; AL121586; CAB89416.1; -;
 CC EMBL; BC032495; AAH32495.1; -;
 CC PIR; A55452; A55452.
 CC PIR; JC2347; JC2347.
 CC HSP; P12643; 3BMP.
 CC Genew; HGNC:4220; GDF5.
 CC MIM; 601146; -;
 CC MIM; 201250; -;
 CC MIM; 200700; -;
 CC GO; GO:0008083; P:growth factor activity; TAS.
 CC GO; GO:0005515; P:protein binding activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0007179; P:TGFbeta receptor signaling pathway; TAS.
 CC InterPro; IPR001839; TGFb.
 CC InterPro; IPR001111; TGFb.N.
 CC Pfam; PF00019; TGF-beta.1.
 CC Pfam; PF00688; TGF-beta; 1.
 CC ProDom; PD000357; TGFb; 1.
 CC SMART; SM00204; TGFb; 1.
 CC PROSITE; PS00250; TGF-BETA.1; 1.
 KW Signal; Growth factor; Cytokine; Glycoprotein; Dwarfism.

FT SIGNAL 1 27 POTENTIAL.
 FT PROPEP 28 381 POTENTIAL.
 FT CHAIN 382 501 GROWTH/DIFFERENTIATION FACTOR 5.
 FT DISULFID 400 466 BY SIMILARITY.
 FT DISULFID 429 498 BY SIMILARITY.
 FT DISULFID 433 500 BY SIMILARITY.
 FT DISULFID 465 465 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 38 38 T -> S (IN REF. 2).
 FT CONFLICT 254 258 APGGG -> VPSR (IN REF. 2).
 FT CONFLICT 276 276 S -> A (IN REF. 2).
 FT CONFLICT 321 321 A -> T (IN REF. 2).
 FT CONFLICT 384 384 L -> S (IN REF. 2).
 FT SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5EF CRC64;
 SQ
 Query Match 99.4%; Score 645; DB 1; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1.2e-61;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKRFPSKNLKARCSKALHVNFKDWDWIIAPLEYAFHCEGLCEPLRSHLE 60
 DB 383 PLATROGKRFPSKNLKARCSKALHVNFKDWDWIIAPLEYAFHCEGLCEPLRSHLE 442
 QY 61 PTNHAVIQTLLNSMDPEPTTACVPTLSPISILFIDSANNVYKQYEDNVVESCGR 119
 DB 443 PTNHAVIQTLLNSMDPEPTTCCVPTLSPISILFIDSANNVYKQYEDNVVESCGR 501
 RESULT 2
 GDF5_MOUSE STANDARD; PRT: 495 AA.
 ID GDF5_MOUSE AC P43027;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 5 precursor (GDF-5).
 GN GDF5 OR GDF-5 OR BP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=94195427; PubMed=8145850;
 RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
 RA Lee S.-J.;
 RT "Inhib. alterations in brachypodism mice due to mutations in a new
 member of the TGF-beta-superfamily.";
 RL Nature 368:639-643(1994).
 CC -|- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -|- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -|- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH
 CC ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE
 CC AXIAL SKELETON.
 CC -|- SIMILARITY: Belongs to the TGF-beta family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U08337; AAA18778.1; -;
 CC PIR; S43294; S43294.
 CC HSP; P12643; 3BMP.
 CC MGD; MGI:956688; Gdf5.
 CC InterPro; IPR001839; TGFb.
 CC InterPro; IPR001111; TGFb.N.
 CC Pfam; PF00019; TGF-beta; 1.
 CC Pfam; PF00688; TGFb_propeptide; 1.

```

DR PRODom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 375 POTENTIAL.
FT CHAIN 376 495 POTENTIAL.
FT DISULFID 394 460 BY SIMILARITY.
FT DISULFID 423 492 BY SIMILARITY.
FT DISULFID 427 494 BY SIMILARITY.
FT DISULFID 459 459 INTERCHAIN (BY SIMILARITY).
FT CAROHVD 183 133 INTERCHAIN (BY SIMILARITY).
FT VARIANT 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 495 AA; 54885 MW; CD005DB48185D2E3 CRC64;

Query Match 98.6%; Score 640; DB 1; Length 495;
Best Local Similarity 98.3%; Pred. No. 4e-61;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROGKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 60
Db 377 PLANROGKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 436

QY 61 PTHNAVITQILMSNDPESTPTACVPTPLSPISILFIDSANNVYKQYEDMVYESGCR 119
Db 437 PTHNAVITQILMSNDPESTPTCCVPTPLSPISILFIDSANNVYKQYEDMVYESGCR 495

RESULT 3
GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN GDF6 OR GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.B.; Huynh T.V.; Copeland N.G.; Jenkins N.A.; Kingsley D.M.;
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
member of the TGF-beta superfamily."
RL Nature 368:639-643(1994).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
DR EMBL; U08338; AAA18779.1; -
DR FTR; S43295; S43295.
DR HSSP; P12643; 3BMP.
DR MGD; MGI:95689; Gdf6.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002403; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBIN.
DR PRODom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein.
FT NON_TER 1 1 POTENTIAL.
FT CHAIN 6 125 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 24 90 BY SIMILARITY.
FT DISULFID 53 122 BY SIMILARITY.
FT DISULFID 57 124 BY SIMILARITY.
FT DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 83.7%; Score 543; DB 1; Length 125;
Best Local Similarity 80.3%; Pred. No. 2e-51;
Matches 94; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATRQGRKPSKNLKARCSRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLEPT 62
Db 9 ASRHGRHKKSLRCSRKPLHVNFKELGDDWIIAPLEYAFHCEGLCEPLRSHLEPT 68

QY 63 NHAVTQILMSNDPESTPTACVPTPLSPISILFIDSANNVYKQYEDMVYESGCR 119
Db 69 NHAVTQILMSNDPESTPTCCVPTPLSPISILFIDSANNVYKQYEDMVYESGCR 125

RESULT 4
GDF6_BOVIN STANDARD; PRT; 436 AA.
AC P55106;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
morphogenetic protein 2) (CDMP-2) (Fragment).
GN GDF6 OR CDMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S.; Hoang B.; Thomas J.T.; Vukicevic S.; Luyten F.P.;
RA Ryba N.J.P.; Kozak C.A.; Reddi A.H.; Moos M.;
RT "Cartilage-derived morphogenetic proteins. New members of the
transforming growth factor-beta superfamily predominantly expressed
in long bones during human embryonic development."
RL J. Biol. Chem. 269:28227-28234(1994).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
DR EMBL; U13661; AAA61416.1; -
DR FTR; B55452; B55452.
DR HSSP; P18075; IBMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein.

```


FT	DISULFID	294	360	BY SIMILARITY.
FT	DISULFID	323	392	BY SIMILARITY.
FT	DISULFID	327	394	BY SIMILARITY.
FT	DISULFID	359	359	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	50	50	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	116	116	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	395 AA;	43837 MW;	OFA3340DFA6360E CRC64;
Query Match				
Best Local Similarity 54.2%; Score 352; DB 1; Length 395;				
Matches 60; Conservative 22; Mismatches 28; Indels 0; Gaps 0;				
QY	10 PSKMLKARSKALHVNFKDMGWDWIIAPLEAYEAFHCEGLCEPFLRSLHLEPTNHAVIQT 69			
DB	286 PTASITWICRHELFVSEFDVGVENWIIAPMGVQAYVCGCEPFLGRLNGTNGHAIQT 345			
QY	70 LMNSDPESTPTACVPTRLPSILFIDSANNVVKYEDVMVESCGR 119			
DB	346 LVNSIDNRAVPKYCCAPTKLSGLSMVLDNNENNVLRQYEDVMVVEAGCR 395			
RESULT 8				
ID	BMP2_RAT	STANDARD;	PRF;	393 AA.
AC	P49001;			
DC	DT 01-FEB-1996 (Rel. 33, Created)			
DT	DT 01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).			
GN	BMP2 OR BMP-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Bone;			
RC	Feng J.O., Chen D., Peng M., Harris M.A., Mundy G.R., Harris S.E.;			
RL	Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.			
CC	-!- SUBUNIT: Homodimer; disulfide-linked.			
CC	-!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.			
CC	-!- SIMILARITY: Belongs to the TGF-beta family.			
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DR	EMBL; 225868; CAA81088.1; -			
DR	FIR; S37073; S37073.			
DR	HSP; P12643; 3BMP.			
DR	InterPro; IPR002405; Inhibin_alpha.			
DR	InterPro; IPR001839; TGFb.			
DR	InterPro; IPR001111; TGFb.N.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	Pfam; PF00688; TGFb_propeptide; 1.			
DR	PRINTS; PR00669; INHIBINA.			
DR	ProDom; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.			
FT	SIGNAL	1	19	POTENTIAL.
FT	PROPEP	20	279	
FT	'CHAIN	280	393	BONE MORPHOGENETIC PROTEIN 2.
FT	DISULFID	293	358	BY SIMILARITY.
FT	DISULFID	322	390	BY SIMILARITY.
FT	DISULFID	326	392	BY SIMILARITY.
FT	DISULFID	357	357	INTERCHAIN (BY SIMILARITY).

[illegible]

DR Pfam: PF00688; TGFb propeptide; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 281 BY SIMILARITY.
 FT CHAIN 282 395 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID 295 360 BY SIMILARITY.
 FT DISULFID 324 392 BY SIMILARITY.
 FT DISULFID 328 394 BY SIMILARITY.
 FT DISULFID 359 359 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 395 AA; 44664 MW; 8D1DDCFBAC582496 CRC64;
 Query Match 53.5%; Score 347; DB 1; Length 395;
 Best Local Similarity 54.3%; Pred. No. 8.Re-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;
 QY 5 RQK-RPSKMLKARCSKALHVNFKDGMWDWIITAPLEYAFHCGLCGCEFFLRSHLEPTN 63
 Db 281 RQAKHKORKRLKSSCKRHLPLVDFSDVGWNDWIYAPPGYHAFYCHGCEFPFLADHLNSTN 340
 QY 64 HAVIQTLMNSMDPESTPPACVPTLSPISILFIDSANNVYKQYEDMVESGCR 119
 Db 341 HAVIQTLMNSVN-SKIPKACCVPTLSAISMLYLDENEKVKLVNKYQDMVVEGCGCR 395
 RESULT 11
 BMP2_DAMDA
 ID BMP2_DAMDA STANDARD; PRT; 396 AA.
 AC G19006;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2).
 GN BMP2.
 OS Dama dama (Fallow deer) (Cervus dama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 OX NCBI_TaxID=30532;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Antler;
 RX MEDLINE=97157076; PubMed=9003457;
 RA Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
 RA Harris S.E.;
 RA "Bone morphogenetic protein 2 transcripts in rapidly developing deer
 RA antler tissue contain an extended 5' non-coding region arising from a
 RA distal promoter.";
 RL Biochim. Biophys. Acta 1350:47-52(1997).
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: A7001817; CAA05033.1; -.
 DR HSSP: PL2643; 3BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGF-beta; 1.

DR Pfam: PF00688; TGFb propeptide; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 282 BY SIMILARITY.
 FT CHAIN 283 396 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID 296 361 BY SIMILARITY.
 FT DISULFID 325 393 BY SIMILARITY.
 FT DISULFID 329 395 BY SIMILARITY.
 FT DISULFID 360 360 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 396 AA; 44646 MW; 5FE23A0AC7F91572 CRC64;
 Query Match 53.5%; Score 347; DB 1; Length 396;
 Best Local Similarity 54.3%; Pred. No. 8.Re-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;
 QY 5 RQK-RPSKMLKARCSKALHVNFKDGMWDWIITAPLEYAFHCGLCGCEFFLRSHLEPTN 63
 Db 282 RQAKHKORKRLKSSCKRHLPLVDFSDVGWNDWIYAPPGYHAFYCHGCEFPFLADHLNSTN 341
 QY 64 HAVIQTLMNSMDPESTPPACVPTLSPISILFIDSANNVYKQYEDMVESGCR 119
 Db 342 HAVIQTLMNSVN-SKIPKACCVPTLSAISMLYLDENEKVKLVNKYQDMVVEGCGCR 396
 RESULT 12
 BMP2_HUMAN
 ID BMP2_HUMAN STANDARD; PRT; 396 AA.
 AC P12643;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
 GN BMP2 OR BMP2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89072730; PubMed=3201241;
 RA Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RA "Novel regulators of bone formation: molecular clones and
 RA activities.";
 RL Science 242:1528-1534(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.;
 RA "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Griffiths R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslahti M., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.I., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Walley D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.
 RX MEDLINE=99175323; PubMed=10074410;
 RA Scheufler C., Sebald W., Huelsmeyer M.,
 RT "Crystal structure of human bone morphogenetic protein-2 at 2.7 A
 resolution.";
 RL J. Mol. Biol. 287:103-115(1999).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND
 CC COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
 CC LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
 CC SMALL INTESTINE.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC
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 DR EMBL; M22489; AAA51834.1; -;
 DR EMBL; AF040249; AAF21645.1; -;
 DR EMBL; AL035668; CAB82007.1; -;
 DR PIR; B37278; BMH02.
 DR PDB; 3BMP; 12-MAR-00.
 DR PDB; 1ES7; 07-OCT-00.
 DR Genew; HGNC:1069; BMP2.
 DR MIM; 112261; -;
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
 KW 3D-structure.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 282
 FT CHAIN 283 396 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID 296 361
 FT DISULFID 325 393
 FT DISULFID 329 395
 FT DISULFID 360 360
 FT CARBOHYD 135 135
 FT CARBOHYD 163 163
 FT CARBOHYD 164 164
 FT CARBOHYD 200 200
 FT CARBOHYD 295 295
 FT STRAND 297 299

FT STRAND 302 304
 FT TURN 305 309
 FT TURN 311 313
 FT STRAND 314 316
 FT STRAND 319 321
 FT STRAND 324 326
 FT STRAND 328 328
 FT TURN 331 332
 FT STRAND 339 339
 FT HELIX 341 352
 FT TURN 354 355
 FT STRAND 361 374
 FT TURN 376 377
 FT STRAND 380 396
 SQ SEQUENCE 396 AA; 44702 MW; 20653A3987B25E60 CRC64;
 Query Match 53.5%; Score 347; DB 1; Length 396;
 Best Local Similarity 54.3%; Pred. No. 8.8e-30;
 Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;
 QY 5 ROGK-RPSKNLKARCSKALHNFYKDMGDDWIIAPLEYAFECBGLCEFFPLRSHLEPTN 63
 DB 282 RQAKHKQRKLKSSCKRHPLYDFSDVGNDWIYAPPGYHAFYCHGCEFPPLADHLNSTN 341
 QY 64 HAVIOTLNSMDPESPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 DB 342 HAIVOTLVNSV-SKIPKACCVPTELSAISMLYLDENEKVLKNTQDMVVECGCR 396
 RESULT 13
 BMP4_XENLA
 ID BMP4_XENLA STANDARD; PRT; 401 AA.
 AC P30895;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 4 precursor (BMP-4).
 GN BMP-4 OR DVR-4.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 ON NCBI_TaxID=8355;
 RX MEDLINE=92378616; PubMed=1510675;
 RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
 RT "Genes for bone morphogenetic proteins are differentially transcribed
 RL in early amphibian embryos.";
 RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93048825; PubMed=1425343;
 RA Jones C.M., Lyons K.M., Lapan P.M., Wright C.V., Hogan B.L.;
 RT "DVR-4 (bone morphogenetic protein-4) as a posterior-ventralizing
 RL factor in Xenopus mesoderm induction.";
 RL Development 115:639-647(1992).
 CC -!- FUNCTION: POSTERIOR-VENTRALIZING FACTOR IN XENOPUS MESODERM
 CC INDUCTION. INDUCES POSTEROVENTRAL MESODERM AND COUNTERACTS
 CC DORSALIZING SIGNALS SUCH AS ACTIVIN.
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC
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 CC
 DR EMBL; X63426; CAA45020.1; -;

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DR PIR; JH0689; JH0689.
DR HSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 287 BY SIMILARITY.
FT CHAIN 288 401 BONE MORPHOGENETIC PROTEIN 4.
FT DISULFID 301 366 BY SIMILARITY.
FT DISULFID 330 398 BY SIMILARITY.
FT DISULFID 334 400 BY SIMILARITY.
FT DISULFID 365 365 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 401 AA; 45988 MW; 3580DEC4B9890047 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 401;
Best Local Similarity 52.1%; Pred. No. 8.9e-30;
Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TRQKRPKNLAKR-----CSRKALHYNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSH 58
Db TRSKRSPKQRPKRKNKCHRRHSLYVDFSDVGNWDWIAPPGYQAFYCHGDCPFPLADH 341
QY 59 LEPTNHAIVOTLNSMDPESTPTACVPTRLSPISILFSDSNANNVYKYEDMVVSCGC 118
Db LNSTNHAIVOTLVNSVNS-SSIPKACCVPTLSAISMILYDEYKVLKNYQEMVVGCGC 400
QY 119 R 119
Db 401 R 401

RESULT 14
DECA_DROSI STANDARD; PRT; 593 AA.
AC P91706;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Decapentaplegic protein precursor (DPP-C protein).
GN DPP.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NET Dpl.
EX MEDLINE=97225212; PubMed=9071595;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL Genetics 145:297-309(1997).
CC -I- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC -I- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT. DPP/DPP
CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED

WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
AND MIDGUT MESODERM (BY SIMILARITY).
-I- SIMILARITY: Belongs to the TGF-beta family.
-----
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-----
CC EMBL; U63854; AAC47554.1; -
DR HSP; P12643; 3BMP.
DR FlyBase; FBgn0015673; Dsim\ddp.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW Signal.
FT SIGNAL 1 15 POTENTIAL.
FT PROPEP 16 461 BY SIMILARITY.
FT CHAIN 462 593 DECAPENTAPLEGIC PROTEIN.
FT DISULFID 492 538 BY SIMILARITY.
FT DISULFID 521 590 BY SIMILARITY.
FT DISULFID 525 592 BY SIMILARITY.
FT DISULFID 557 557 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 593 AA; 66248 MW; F0DBE21209F44380 CRC64;

Query Match 53.5%; Score 347; DB 1; Length 593;
Best Local Similarity 49.6%; Pred. No. 1.4e-29;
Matches 58; Conservative 24; Mismatches 33; Indels 2; Gaps 1;

QY 5 RQKRP--KNLKARCSRKALHYNFKDMGWDWIIAPLEYAFHCEGLCEFFLRSHLEPT 62
Db RQRPRTREKNHDDTCRRHSLYVDFSDVGNWDWIAPPLGYDAYTYCHGKCPFLADHFNST 536
QY 63 NHAIVOTLNSMDPESTPTACVPTRLSPISILFSDSNANNVYKYEDMVVSCGCR 119
Db NHAIVOTLVNNMNPCKVPRACCVPTQLDSVAMLYLNDQSTVVLKNYQEMVVGCGCR 593

RESULT 15
BMP4_CHICK
ID BMP4_CHICK STANDARD; PRT; 405 AA.
AC Q90752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 4 precursor (BMP-4).
GN BMP4 OR BMP-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RT patterning in the developing chick limb.";
RL Development 120:209-218(1994).
RN [2]
```

RP FUNCTION.
RX MEDLINE=99128179; PubMed=9927590;
RA "Pizette S., Niswander L.;
RT "BMPs negatively regulate structure and function of the limb apical
RL ectodermal ridge.";
RL Development 126:883-894(1999).
CC -!- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE
CC LIMB APICAL ECTODERMAL RIDGE.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
DR EMBL: X75915; CAA53514.1; -.
DR PIR: I50608; I50608.
DR HSSP: PI2643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR ProDom: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 291 BY SIMILARITY.
FT CHAIN 292 405 BONE MORPHOGENETIC PROTEIN 4.
FT DISULFID 305 370 BY SIMILARITY.
FT DISULFID 334 402 BY SIMILARITY.
FT DISULFID 338 404 BY SIMILARITY.
FT DISULFID 369 369 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 405 AA; 46057 MW; 544302D8A0A40F81 CRC64;

Query Match 53.3%; Score 346; DB 1; Length 405;
Best Local Similarity 52.1%; Pred. No. 1.2e-29;
Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TROGKP-----SKNLKRCRKALHVNFKMGWDDWIIADLEYAPHCEGLCEPFLRSH 58
DB 286 TRARRSPKHGSRKKNKCRKHALYDFSDYGNWDIVAPPGYQAFYCHGDCPPFLADH 345

QY 59 LEPTNHAVIQTLNMSDPPPTPACVPTRLSPISLFTDSANNVYKQEDAVVESGCG 118
DB 346 LNSTNHAVIQTLVNSVN-SSIPKACCVPTLSAISMLYLDYDKVLKNYQENMYVEGCGC 404

QY 119 R 119
DB 405 R 405

Search completed: September 26, 2003, 17:57:14
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: September 26, 2003, 17:53:21 : Search time 97 Seconds
(without alignments)
316.580 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATQGRKPSKLNKARCSR.....ANNVYKQYEDMVVSCGCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	98.6	249	11 Q8BRW9	Q8brw9 mus musculus
2	637	98.2	500	13 Q9W6G0	Q9w6g0 gallus gall
3	587	90.4	324	13 Q9YHW9	Q9yhw9 gallus gall
4	563	86.7	257	13 Q42303	O42303 brachydanio
5	534.5	82.4	126	13 Q93573	Q93573 gallus gall
6	527.5	81.3	261	13 Q9W6C0	Q9w6c0 brachydanio
7	527	81.2	413	13 Q9DGN4	Q9dgn4 xenopus lae
8	524	80.7	399	13 Q9W753	Q9w753 xenopus lae
9	524	80.7	412	13 Q12938	Q12938 brachydanio
10	491	75.7	294	6 Q9BDW9	Q9bdw9 macaca fasc
11	491	75.7	447	6 Q9BDW8	Q9bdw8 cercopithec
12	386	59.5	441	11 Q99NY1	Q99ny1 mus musculus
13	368.5	56.8	361	5 Q96504	Q96504 brachiosteo
14	368	56.7	204	5 Q9XZ69	Q9xz69 tripneustes
15	366	56.4	411	5 Q9U418	Q9u418 brachiosteo
16	365	56.2	405	5 Q9U5E8	Q9u5e8 ptychodera

17	361	55.6	289	5 Q9XYQ8	Q9xyq8 strongyloce
18	359	55.3	417	5 Q9XYQ7	Q9xyq7 lytechinus
19	357.5	55.1	509	5 Q8WS99	Q8ws99 archaster t
20	357	55.0	67	11 Q8K4X5	Q8k4x5 rattus norv
21	355.5	54.8	178	5 Q25211	Q25211 junonia coe
22	355.5	54.8	461	5 Q8MX23	Q8mx23 hemicentrot
23	354	54.5	67	6 Q02783	Q02783 bos taurus
24	350	53.9	277	13 Q90Y82	Q90y82 lampera ja
25	349.5	53.9	411	13 Q57573	Q57573 brachydanio
26	349.5	53.9	411	13 Q93369	Q93369 brachydanio
27	348	53.6	398	13 Q90YD7	Q90yd7 xenopus tro
28	347.5	53.5	128	5 Q95W38	Q95w38 schistocerc
29	347	53.5	588	5 Q9VOC6	Q9vgc6 drosophila
30	346	53.3	400	13 Q73818	Q73818 xenopus lae
31	346	53.3	400	13 Q91703	Q91703 xenopus lae
32	346	53.3	443	5 Q76851	Q76851 halocynthia
33	345	53.2	400	13 Q90YD6	Q90yd6 xenopus tro
34	344.5	53.1	411	13 Q13108	Q13108 brachydanio
35	343	52.9	378	5 Q8MXC2	Q8mxc2 acropora mi
36	342.5	52.8	191	5 Q26468	Q26468 schistocerc
37	342	52.7	373	13 Q98950	Q98950 gallus gall
38	342	52.7	373	13 Q90723	Q90723 gallus gall
39	342	52.7	400	13 Q57574	Q57574 brachydanio
40	342	52.7	407	5 Q8MWG4	Q8mwg4 patella vul
41	341	52.5	422	5 Q8IAE3	Q8iae3 stichopus j
42	340	52.4	400	13 Q13107	Q13107 brachydanio
43	340	52.4	403	13 Q8JIK0	Q8jik0 cyprichromi
44	340	52.4	403	13 Q8J1J7	Q8j1j7 julidochrom
45	340	52.4	403	13 Q8J1J4	Q8j1j4 steatocranu

ALIGNMENTS

RESULT 1

Q8BRW9	PRELIMINARY;	PRT;	249 AA.
AC	Q8BRW9		
DT	01-MAR-2003 (TREMREL. 23, Created)		
DT	01-MAR-2003 (TREMREL. 23, Last sequence update)		
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)		
DE	Growth differentiation factor 5 (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Aorta and vein;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573(2002).		
DR	EMBL; AK041168; BAC30847.1; -.		
FT	NON TER		
SQ	SEQUENCE 249 AA; 28409 MW; E6EA047F06B57189 CRC64;		

Query Match 98.6%; Score 640; DB 11; Length 249;

Best Local Similarity 98.3%; Pred. No. 1.7e-67;

Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQGRKPSKLNKARCSRKALHVFNKDMGDDWIIAPLEVFHCEGCEPLRSHLE 60

131 PLATQGRKPSKLNKARCSRKALHVFNKDMGDDWIIAPLEVFHCEGCEPLRSHLE 190

61 PTNHAVIQTLNMSMDPSTPTACVTRLSPTLSILFIDSANNVYKQYEDMVVSCGCR 119

191 PTNHAVIQTLNMSMDPSTPTCCVTRLSPTLSILFIDSANNVYKQYEDMVVSCGCR 249

RESULT 2

<hr/>					
Q9W6G0	ID	Q9W6G0	PRELIMINARY;	PRT;	500 AA.
AC	AC	Q9W6G0;			
DT	DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DE	DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	DE	GDF-5 protein.			
GN	GN	GDF5.			
OS	OS	Gallus gallus (Chicken).			
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	OC	Gallus.			
ON	ON	NCBI_TaxID=9031;			
RN	RN	[1]			
RP	RP	SEQUENCE FROM N.A.			
RX	RX	MEDLINE=99146893; PubMed=10021348;			
RA	RA	Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,			
RA	RA	Ladher R., Allen S., Macpherson S., Luyten F.P., Archer C.W.,			
RT	RT	"Mechanisms of Gdf-5 action during skeletal development.";			
RL	RL	Development 126:1305-1315(1999).			
RC	RC	-/- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	DR	EMBL; AF1233389; RAD30451.1; -.			
DR	DR	HSSP; PI2643; 3BMP.			
DR	DR	InterPro; IPR002400; GF_cysknot.			
DR	DR	InterPro; IPR002405; Inhibin_alpha.			
DR	DR	InterPro; IPR001839; TGfb.			
DR	DR	InterPro; IPR001111; TGfb.N.			
DR	DR	Pfam; PF000019; TGfb-beta: 1.			
DR	DR	Pfam; PF00688; TGfb_propeptide; 1.			
DR	DR	PRINTS; PR00438; GFCYSNOT.			
DR	DR	PROSITE; PR00669; INHIBINA.			
DR	DR	PRODOM; PD000357; TGfb; 1.			
DR	DR	SMART; SM00204; TGFB; 1.			
DR	DR	PROSITE; PS00250; TGF.BETA.1; 1.			
SQ	SQ	SEQUENCE 500 AA; 55952 MW; 1DB3895A3119A598 CRC64;			
<hr/>					
Query Match		98.2%; Score 637; DB 13; Length 500;			
Best Local Similarity		97.5%; Pred.No. 8.6e-67;			
Matches 116; Conservative		1; Mismatches 2; Indels 0; Gaps 0;			
<hr/>					
QY	1	PLATROGRKPSKNLKARCSPKALHVNFKDGMDDWIAPLEYEAPHCGICFFPIRSHLE 60			
Db	382	PLATROGRKPSKNLKPCRSRRALHVNFKDGMDDWIAPLEYEAPHCGICFFPIRSHLE 441			
<hr/>					
QY	61	PTNHAVIQTIAMNSDPSTPTTACVPTRLSPISILFIDSANNVVVKQYEDMNVVSCGCR 119			
Db	442	PTNHAVIQTIAMNSDPSTPTTCVCVTRLSPISILFIDSANNVVVKQYEDMNVVSCGCR 500			
<hr/>					
RESULT 3					
Q9YHW9	ID	Q9YHW9	PRELIMINARY;	PRT;	324 AA.
AC	AC	Q9YHW9;			
DT	DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DE	DE	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)			
DE	DE	Growth differentiation factor 5 (Fragment).			
OS	OS	Gallus gallus (Chicken).			
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	OC	Gallus.			
ON	ON	NCBI_TaxID=9031;			
RN	RN	[1]			
RP	RP	SEQUENCE FROM N.A.			
RX	RX	TISSUE-Leg bud;			
RX	RX	MEDLINE=99119368; PubMed=9918693;			
RA	RA	Merino R., MacIas D., Ganay X., Economides A.N., Wang X., Wu Q.,			
RA	RA	Stahl N., Sampath K.T., Varona P., Hurlé J.M.,			
RT	RT	"Expression and function of Gdf-5 during digit skeletogenesis in the			
RT	RT	embryonic chick leg bud;"			
RL	RL	Dev. Biol. 206:33-45(1999).			
CC	CC	-/- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	DR	EMBL; AF075441; AAD14568.1; -.			

QY	66	VIQFLNMSMDPSTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR	119	
DB	204	LIQTLNMSMDPSTPTTCCVPTRLSPISILYIDSANNVYKQYEDMVVSCGCR	257	
RESULT 5				
ID	093573	PRELIMINARY;	PRT;	126 AA.
AC	093573;			
DT	01-NOV-1998	(TREMBlrel. 08, Created)		
DT	01-NOV-1998	(TREMBlrel. 08, Last sequence update)		
DT	01-OCT-2002	(TREMBlrel. 22, Last annotation update)		
DE		Putative growth/differentiation factor 6/7 (Fragment).		
GN	GDF6/7.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=99026113; PubMed=9808626;			
RA	Lee K.J., Mendelsohn M., Jessell T.M.;			
RT	"Neuronal patterning by BMPs: a requirement for GDF7 in the generation			
RT	of a discrete class of commissural interneurons in the mouse spinal			
RT	cord."			
RL	Genes Dev. 12:3394-3407(1998).			
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL; AF089086; AAC97113.1; -.			
DR	HSSP; P12643; 3BMP.			
DR	InterPro; IPR002400; GF_cysknot.			
DR	InterPro; IPR002405; Inhibin_alpha.			
DR	InterPro; IPR001839; TGFb.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	PRINTS; PR00438; GFCYSKNOT.			
DR	PRINTS; PR00669; INHIBINA.			
DR	PRODOM; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
FT	NON_TER			
FT	1			
SQ	SEQUENCE	126 AA;	14265 MW;	CB824D280F44A394 CRC64;
Query Match 82.4%; Score 534.5; DB 13; Length 126;				
Best Local Similarity 79.0%; Pred. No. 2.4e-55;				
Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;				
QY	2	LATQGRK-PSKNLKARCSRKALHVNFKDMGDDWIAPLEYAFHCEGLCEPFLSHLE	60	
DB	8	IPANSRGHGKHKAKYCRSKPLHVNFKELGDDWIAPLDYEAHCEGCDPFLSHLE	67	
QY	61	PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR	119	
DB	68	PTNHAIQTLMNSMDPESTPPSCVPSKLSPLISILYIDSGNNVYKQYEDMVVTCGR	126	
RESULT 6				
ID	Q9W6C0	PRELIMINARY;	PRT;	261 AA.
AC	Q9W6C0;			
DT	01-NOV-1999	(TREMBlrel. 12, Created)		
DT	01-NOV-1999	(TREMBlrel. 12, Last sequence update)		
DT	01-OCT-2002	(TREMBlrel. 22, Last annotation update)		
DE		Growth/differentiation factor 7 (Fragment).		
GN	GDF7.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=99148135; PubMed=10022976;			

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KW Signal.
FY SIGNAL.
SQ SEQUENCE 1 23 POTENTIAL.
Query Match 81.2%; Score 527; DB 13; Length 413;
Best Local Similarity 77.3%; Pred. No. 7.3e-54;
Matches 92; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 PLATQGRKPKNLKARCSKALHVNFKDGMWDWIAPLEYAFHCEGLCEFPRLSHLE 60
DB 295 PRTNGKHGAKKSKTKCSKKPLVNFKELGWDWIAPLEYAHCEGVCDPFLRSHLE 354

QY 61 PTHAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 355 PTHAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 413

RESULT 8
QY753 PRELIMINARY; PRT; 399 AA.
AC QY753;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Growth and differentiation factor 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C., Hemmati-Brivanlou A.;
RL "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF155125; AAD38402.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknnot.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C., Hemmati-Brivanlou A.;
RL "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF155125; AAD38402.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknnot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B5088517 CRC64;

Query Match 80.7%; Score 524; DB 13; Length 399;
Best Local Similarity 77.6%; Pred. No. 1.6e-53;
Matches 90; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 4 TRQGRKPKNLKARCSKALHVNFKDGMWDWIAPLEYAFHCEGLCEFPRLSHLEPTN 63
DB 284 SRHGKHGKSKRLCSKKPLHVNFKELGWDWIAPLEYAHCEGVCDPFLRSHLEPTN 343

QY 64 HAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 344 HAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 399

RESULT 9
O12938 PRELIMINARY; PRT; 412 AA.
AC O12938;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

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DE Dynamo protein precursor.
GN GDF6A OR DYNAMO.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97231294; PubMed=9076689;
RA Bruneau S., Rosa F.;
RL "Dynamo a new zebrafish DVR member of the TGF-B superfamily is expressed in the posterior neural tube and is up regulated by Sonic hedgehog.";
RL Mech. Dev. 61:199-212(1997).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; X99769; CAA68102.1; -.
DR HSSP; P12643; 3BMP.
DR ZFIN; ZDB-GENE-980526-442; gdf6a.
DR InterPro; IPR002400; GF_cysknnot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBIN.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 17 POTENTIAL.
SQ SEQUENCE 412 AA; 47072 MW; 4076E262C4481121 CRC64;

Query Match 80.7%; Score 524; DB 13; Length 412;
Best Local Similarity 74.6%; Pred. No. 1.6e-53;
Matches 88; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 2 LATQGRKPKNLKARCSKALHVNFKDGMWDWIAPLEYAFHCEGLCEFPRLSHLEP 61
DB 295 LPNRHGRKHGKSKRCSKKPLHVNFKELGWDWIAPLEYAHCEGVCDPFLRSHLEP 354

QY 62 TNHAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
DB 355 TNHAVIOTLNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 412

RESULT 10
Q9BDW9 PRELIMINARY; PRT; 294 AA.
AC Q9BDW9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Cerebral cortex motor area;
RX MEDLINE=21136583; PubMed=11238730;
RA Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RL "Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.

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DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 1
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27AF39F CRC64;

Query Match
Best Local Similarity 73.5%; Score 491; DB 6; Length 294;
Matches 83; Conservative 19; Mismatches 11; Indels 0; Gaps 0;

QY 7 GKPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFPRLSHLEPTNHAV 66
Db 182 GRGHRGRGRSRSRKLPHVDFKELGWDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAI 241
QY 67 IOTLNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 242 IOTLNSMAPDAAPASCCVPAFLSPISILYIDAANNVVKQYEDMVVESCGR 294

RESULT 11
Q9BDW8 PRELIMINARY; PRT; 447 AA.
AC Q9BDW8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Growth/differentiation factor 7 is preferentially expressed in the
DE primary motor area of the monkey neocortex."
DE Growth/differentiation factor 7.
GN GDF7.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21136583; PubMed-11238730;
RA Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex."
RL J. Neurochem. 76:1455-1464(2001).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254569; AAK30842.1; -.
DR EMBL; AF254568; AAK30842.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 1
SQ SEQUENCE 447 AA; 46866 MW; DF46D591925A8391 CRC64;

Query Match
Best Local Similarity 75.7%; Score 491; DB 6; Length 447;
Matches 83; Conservative 19; Mismatches 11; Indels 0; Gaps 0;

QY 7 GKPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFPRLSHLEPTNHAV 66
Db 335 GRGHRGRGRSRSRKLPHVDFKELGWDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAI 394
QY 67 IOTLNSMDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
Db 395 IOTLNSMAPDAAPASCCVPAFLSPISILYIDAANNVVKQYEDMVVESCGR 447

RESULT 12
Q99MY1 PRELIMINARY; PRT; 441 AA.
ID Q99MY1

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AC Q99MY1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
GN GDF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tt2;
RX MEDLINE-21136583; PubMed-11238730;
RA Watakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex."
RL J. Neurochem. 76:1455-1464(2001).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254571; AAK30843.1; -.
DR EMBL; AF254570; AAK30843.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 441
SQ SEQUENCE 441 AA; 45617 MW; 74DA312A853701F0 CRC64;

Query Match
Best Local Similarity 59.5%; Score 386; DB 11; Length 441;
Matches 64; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 7 GKPSKNLKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFPRLSHLEPTNHAV 66
Db 349 GRGHRGRGRSRSRKLPHVDFKELGWDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAI 408
QY 67 IOTLNSMDPESTPTACVPTRLSPISILFIDS 99
Db 409 IOTLNSMAPDAAPASCCVPAFLSPISILYIDA 441

RESULT 13
O96504 PRELIMINARY; PRT; 361 AA.
AC O96504;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein 2/4.
GN BMP2/4.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98401944; PubMed-9733108;
RA Panopoulou G.D., Clark M.D., Holland L.Z., Lehrach H., Holland N.D.;
RT "AmphibMP2/4, an amphioxus bone morphogenetic protein closely related
RT to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
RT into evolution of dorsoventral axis specification."
RL Dev. Dyn. 213:130-139(1998).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF068750; AAC97488.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.

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DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom: PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 361 AA; 41517 MW; 09FF5FE6C9785DD1 CRC64;

Query Match 56.8%; Score 368.5; DB 5; Length 361;
Best Local Similarity 52.0%; Pred. No. 3.6e-35;
Matches 64; Conservative 25; Mismatches 29; Indels 5; Gaps 1;

QY 2 LATRQ-----GKRPSKMLKARCSKALHVNFKDMGWDWIAPLEYEAFHCEGLCEPFLR 56
DB 239 VASRQKRANGKRORRLKANCRRHSLYDFSDVGNWDWIIVAPPGYQAYICHGECFFPLA 298
QY 57 SLEPTNHAIVQTLNMSMDPEPTACVPTRLSPISILFDSANNVYKQYEDMAYVESC 116
DB 299 DHLNSNHAIVQTLVNSVNPAYPKACCVPTDLSFISMLYLINENDQVVLKNYQDMAYVESC 358
QY 117 GCR 119
DB 359 GCR 361

RESULT 14
QYXZ69 PRELIMINARY; PRT; 204 AA.
AC Q9XZ69;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein 2/4 homolog (Fragment).
GN BMP2/4.
OS Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopneuroidea; Toxopneustidae;
OC Tripneustes.
OX NCBI_TaxID=7673;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99262121; PubMed=10329409;
RX Hwang S.L., Chen C.A., Chen C.;
RT "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RT closely related to vertebrate BMP2 and BMP4 with maximal expression at
RT the later stages of embryonic development.";
RL Biochem. Biophys. Res. Commun. 258:457-463(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF133305; AAD30538.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 1
SQ SEQUENCE 204 AA; 23697 MW; CE829BDC2AA9F077 CRC64;

Query Match 56.7%; Score 368; DB 5; Length 204;
Best Local Similarity 53.8%; Pred. No. 2.2e-35;
Matches 63; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 3 ATROGKRPSKMLKARCSKALHVNFKDMGWDWIAPLEYEAFHCEGLCEPFLRSHLEPT 62
DB 88 SSRSRKRKGRLLKANCRRHPLYDFSDVHNDWIIVAPAGYQAYICHGECFFPLAHLNLT 147
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QY 63 NHAIVQTLNMSMDPEPTACVPTRLSPISILFDSANNVYKQYEDMAYVESCGR 119
DB 148 NHAIVQTLVNSVNPALVPKACCVPTDLSAISMLYLDEYKVLKNYQDMAYVESCGR 204

RESULT 15
QYU418 PRELIMINARY; PRT; 411 AA.
ID Q9U418;
AC Q9U418;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bone morphogenetic protein 2/4.
GN BMP2/4.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasui K., Saiga H., Uemura M., Samba I.;
RT "Early body formation and expression pattern of genes encoding
RT secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF206325; AAF19841.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 411 AA; 46929 MW; F579898060F18355 CRC64;

Query Match 56.4%; Score 366; DB 5; Length 411;
Best Local Similarity 53.0%; Pred. No. 8.3e-35;
Matches 62; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

QY 3 ATROGKRPSKMLKARCSKALHVNFKDMGWDWIAPLEYEAFHCEGLCEPFLRSHLEPT 62
DB 295 ANGRKKHORRLKANCRRHSLYDFSDVGNWDWIIVAPPGYQAYICHGECFFPLADHLNST 354
QY 63 NHAIVQTLNMSMDPEPTACVPTRLSPISILFDSANNVYKQYEDMAYVESCGR 119
DB 355 NHAIVQTLVNSVNPALVPKACCVPTDLSFISMLYLINENDQVVLKNYQDMAYVESCGR 411
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Search completed: September 26, 2003, 17:59:01
Job time : 101 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2003, 17:42:43 ; Search time 84 Seconds
(without alignments)
224.863 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649
Sequence: 1 PLATROGKPSKNLKARCSR.....ANNVYKQYEDMVVESCGR 119

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	649	100.0	119	21	AY44296	Mutant human MP52
2	645	99.4	119	17	AAW06920	Human MP52 growth
3	645	99.4	119	18	AAW19846	Human bone inducin
4	645	99.4	120	16	AAW78731	Murine protein MP5
5	645	99.4	120	18	AAW26590	Human MP52 protein
6	645	99.4	120	22	AAE10973	Human MP-52 protel
7	645	99.4	120	24	ABG73290	Amino acid sequenc
8	645	99.4	401	14	AAW40800	TGF-beta-like clon
9	645	99.4	501	16	AAW69600	New TGF-beta famil

10	645	99.4	501	18	AAW36100	Human MP52. Homo
11	645	99.4	501	18	AAW19210	Human TGF-beta pro
12	645	99.4	501	18	AAW11900	Human high mol. wt
13	645	99.4	501	18	AAW01799	Human MP52 protein
14	645	99.4	501	18	AAW12770	Human bone morphog
15	645	99.4	501	19	AAW44868	TGF-beta superfami
16	645	99.4	501	19	AAW33008	Human MP52. Homo
17	645	99.4	501	22	AAW70529	Human TGF-beta MP5
18	640	98.6	495	15	AAW60022	Growth differentia
19	640	98.6	495	22	AAW84550	Amino acid sequenc
20	640	98.6	495	24	ABG76018	Mouse growth diffe
21	639	98.5	119	21	AAW70752	Wild type mature h
22	639	98.5	119	21	AAW70756	Methionine oxidise
23	639	98.5	119	21	AAW70757	Methionine alkylat
24	639	98.5	119	21	AAW70758	Tryptophan allylsu
25	639	98.5	120	23	AAW51932	Human TGFbeta prot
26	639	98.5	501	17	AAW92034	Cartilage-derived
27	639	98.5	501	21	AAW92034	Human growth diffe
28	559	86.1	102	21	AAW09553	Human CMP-1/GDF-5
29	559	86.1	102	21	AAW02819	Human CMP-1/GDF-5
30	559	86.1	102	21	AAW92578	Human CMP-1/GDF-5
31	543	83.7	120	23	AAW51933	Murine TGFbeta pro
32	543	83.7	125	24	ABG76037	Human GDF-6 C-term
33	543	83.7	134	16	AAW66867	GDF-6. Mus sp. A
34	543	83.7	134	21	AAW12986	Murine growth diff
35	543	83.7	263	16	AAW78739	Murine mv2 protein
36	543	83.7	263	18	AAW26595	Human BMP-13 homo
37	540	83.2	321	16	AAW78730	Human mature VI-1
38	540	83.2	321	18	AAW26591	Human bone morphog
39	540	83.2	321	22	AAE10982	Human full length
40	540	83.2	321	24	ABG73298	Human bone morphog
41	540	83.2	455	22	AAW50216	Human growth/diffe
42	540	83.2	455	23	AAW79173	Human growth/diffe
43	540	83.2	455	23	AAE17604	Human extracellula
44	538	82.9	263	22	AAE10985	Murine partial mv2
45	538	82.9	263	24	ABG73301	Amino acid sequenc

ALIGNMENTS

RESULT 1

AY44296

ID AY44296 standard; Protein; 119 AA.

AC AY44296;

XX

DT 29-FEB-2000 (first entry)

XX

DE Mutant human MP52 monomer protein.

XX

KW Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta;

KW pKOR279 expression vector; osteocyte; bone morphogenetic; osteopathic;

KW anti-arthritis activity; cartilage; osteoporosis; osteoarthritis;

KW arthrostetis; fracture; achondroplasia; dyschondrogenesis;

KW achondrogenesis; palatoschisis; dysosteogenesis.

XX

OS Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers

FT Misc-difference 83 /note= "Wild-type Cys replaced by Ala"

FT

XX

PN WO961611-Al.

XX

PD 02-DEC-1999.

XX

PF 14-MAY-1999; 99WO-IB00866.

XX

PR 22-MAY-1998; 98JP-0141379.

XX

PA (HMRI) HOECHST MARTON ROUSSEL LTD.

XX Kawai S, Kimura M, Muraki Y, Katsuura M;
 XX WPI; 2000-097122/08.
 DR N-PSDB; AA229328.
 XX Novel monomer protein used for prevention and treatment of bone and/or
 PT cartilage diseases -
 PT Claim 4; Page 20; 26pp; English.
 XX The present sequence is a mutant human MP52 monomer protein, which
 CC belongs to transforming growth factor-beta (TGF-beta)
 CC superfamily. Mutant MP52 can be produced in E. coli cells by
 CC transforming them with pK01279 expression vector containing a mutated
 CC MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is
 CC capable of inducing differentiation in osteocytes and exhibits bone
 CC morphogenetic, osteopathic and anti-arthritis activity. The MP52 monomer
 CC protein is used for prevention and treatment of cartilage and/or bone
 CC diseases such as osteoporosis, osteoarthritis, arthrosclerosis, damage of
 CC cartilage, regeneration of bone, cartilage deficit caused by injury and
 CC tumour dissection, fracture, congenital bone and/or cartilage diseases
 CC such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis
 CC and dysostegenesis and a deficit of root of teeth and a tooth socket.
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 649; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 6.9e-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLATGKRPKNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 60
 DB 1 PLATGKRPKNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 60
 QY 61 PTNHAIVQTLNMSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 DB 61 PTNHAIVQTLNMSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 RESULT 2
 AAW06920
 ID AAW06920 standard; Protein; 119 AA.
 AC AAW06920;
 DT 27-JUN-1997 (first entry)
 DE Human MP52 growth factor residues 383-501.
 XX Human; MP52; growth factor; monomer; dimer; treatment; bone;
 KW cartilage; dental; disorder; fracture; bone loss;
 KW periodontal disease; calcification; osteoporosis.
 XX Homo sapiens.
 XX WO9633215-A1.
 PN 24-OCT-1996.
 XX 19-APR-1996; 96WO-JP01062.
 XX 17-NOV-1995; 95JP-0322403.
 PR 19-APR-1995; 95JP-0093664.
 XX (FARH) HOECHST JAPAN LTD.
 PA Enomoto K, Katsuura M, Kawai S, Kimura M, Makishima F;
 PI Matsumoto T, Miki, Satoh Y, Takamatsu H;
 XX WPI; 1996-485730/48.
 DR N-PSDB; AAT46150.
 XX

PT Peptide consisting of part of human MP52 growth factor, and its
 PT dimer - is used for treatment of bone, cartilage and dental
 PT disorders
 XX Claim 1; Pages 18-19; 33pp; Japanese.
 XX The present sequence is residues 383 to 501 of the human MP52
 CC growth factor, a dimer of which can be used to treat bone,
 CC cartilage and dental disorders, including fractures, bone loss and
 CC periodontal disease. The dimer was prepared by transforming a host
 CC (preferably E. coli) with a suitable (plasmid) expression vector
 CC containing DNA encoding the monomer. The host was cultured, and
 CC inclusion bodies from the cells worked up to give the monomer,
 CC which was then converted into the dimer. The product was mixed with
 CC type 1 pig tendon collagen and injected into the large thigh vein
 CC of ICR mice. After 20 days 4 of 4 mice injected with 10 microg of
 CC the dimer showed bone/cartilage calcification around the injection
 CC site, compared to none in 0 of 4 mice treated with collagen only.
 XX Sequence 119 AA;
 SQ Query Match 99.4%; Score 645; DB 17; Length 119;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATGKRPKNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 60
 DB 1 PLATGKRPKNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHLE 60
 QY 61 PTNHAIVQTLNMSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 DB 61 PTNHAIVQTLNMSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 RESULT 3
 AAW19846
 ID AAW19846 standard; Protein; 119 AA.
 XX AAW19846;
 DT 12-FEB-1998 (first entry)
 DE Human bone inducing factor MP52.
 XX Human; bone inducing factor; MP52; collagen; fracture;
 KW polyoxyethylene-polyoxypropylene glycol.
 XX Homo sapiens.
 XX WO9718829-A1.
 PN 29-MAY-1997.
 XX 14-NOV-1996; 96WO-JP03333.
 XX 17-NOV-1995; 95JP-0322402.
 XX (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST PHARM & CHEM KK.
 XX Shimura T, Toriyama S;
 PI WPI; 1997-310243/28.
 DR N-PSDB; AAT70296.
 XX Material for repairing bone and collagen, especially bone fracture
 PT or loss - comprising bone-inducing factor and
 PT polyoxyethylene-polyoxypropylene glycol compounds
 XX Example 4; Page 16-17; 31pp; Japanese.
 XX Bone and collagen inducing material has been developed which comprises
 CC bone inducing factor and polyoxyethylene-polyoxypropylene glycol

CC compounds. The present sequence represents human bone inducing factor
 CC MP52. This material allows treatment without surgery. It is highly
 CC absorbable because a carrier is used with the bone inducing factor,
 CC and undergoes reversible sol-gel transition depending on the
 CC temperature.
 XX
 SQ Sequence 119 AA;

Query Match 99.4%; Score 645; DB 18; Length 119;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRSKMLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLE 60
 DB 1 PLATROGKRSKMLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLE 60
 QY 61 PTNHAVIQTILMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
 DB 61 PTNHAVIQTILMNSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119

RESULT 4
 AAR78731
 ID AAR78731 standard; Protein; 120 AA.
 XX
 AC AAR78731;
 DT 25-MAR-2003 (updated)
 DT 23-NOV-1995 (first entry)
 XX Murine protein MP52.
 XX Bone morphogenetic protein; MP52; tendon; ligament.
 XX Mus musculus.
 XX WO9516035-A2.
 PD 15-JUN-1995.
 XX 06-DEC-1994; 94WO-0514030.
 XX 02-NOV-1994; 94US-0333576.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 XX (GENY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX WPI; 1995-2243320/29.
 DR N-PSDB; AAQ96209.
 XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 PT compsn. for inducing tendon/ligament-like tissue formation
 XX Example; Page 51-52; 84pp; English.
 XX Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
 CC amplification of a 275 bp DNA probe, the internal 269 bp of which
 CC corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding
 CC plasmid subclone PCR1-1#2. This probe was radioactively labelled
 CC and used to screen a murine genomic library. DNA sequence analysis
 CC of one of positively hybridising recombinants named MVR23 indicates
 CC that it encodes a portion of the mouse gene corresp. to the PCR
 CC product mV9 (murine homolog of the MP-52 sequence AAQ96209/R78731).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 16; Length 120;

Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRSKMLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLE 60
 DB 2 PLATROGKRSKMLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLE 61
 QY 61 PTNHAVIQTILMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
 DB 62 PTNHAVIQTILMNSMDPESTPTTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120

RESULT 5
 AAW26590
 ID AAW26590 standard; Protein; 120 AA.
 XX
 AC AAW26590;
 DT 25-MAR-2003 (updated)
 DT 21-JAN-1998 (first entry)
 XX Human MP52 protein.
 XX MP52; BMP; bone morphogenetic protein; human; tendon; ligament;
 KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
 KW therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Protein 1..120
 FT Protein /note= "Claim 5"
 FT Protein 19..120
 FT Protein /note= "Claim 5"
 XX US658882-A.
 PN 19-AUG-1997.
 XX 22-DEC-1994; 94US-0362670.
 XX 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX (GENY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX WPI; 1997-424270/39.
 DR Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
 PT - useful for tissue healing and repair, treatment of tendonitis,
 PT improving fixation of tendons to bone etc
 XX Claim 5; Column 39-40; 43pp; English.
 XX This polypeptide comprises human MP52. A claimed method for
 CC inducing formation of tendon and/or ligament tissues involves the
 CC administration of a composition containing at least one protein
 CC selected from MP52, BMP-12 (see AAW26589) and BMP-13 (see AAW26591).
 CC The method is used for tissue (including skin) healing and repair.
 CC This is useful for treating tendonitis, carpal tunnel syndrome and
 CC other defects of traumatic or congenital origin, in cosmetic
 CC surgery and to improve fixation of tendons or ligaments to bone.
 CC The specified proteins can also be used to increase activity of other
 CC BMPs e.g. BMP-2 (see AAW26597).
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 18; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 |||||||
 Db 2 PLATROGKRPSSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61
 |||||||

QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
 |||||||
 Db 62 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120
 |||||||

RESULT 6
 AAEL0973
 ID AAEL0973 standard; Protein; 120 AA.
 XX
 AC AAEL0973;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human MP-52 protein.
 XX
 KW Human; MP-52; vulnary; antiinflammatory; analgesic; ligament defect;
 KW transforming growth factor-beta; TGF-beta; tissue formation; tendonitis;
 KW wound healing; tissue repair; carpal tunnel syndrome; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6284872-B1.
 PD 04-SEP-2001.
 XX
 PF 28-FEB-1997; 97US-0808324.
 XX
 PR 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX
 PA (GENY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 WPI; 2001-588978/66.
 DR N-PFDB; AAD18317.
 XX
 PT New chimeric DNAs, useful for treating tendonitis, carpal tunnel
 PT syndrome and other tendon and ligament defects, comprises DNA encoding
 PT propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
 PT BMP-13 or MP52 -
 XX
 PS Disclosure; Column 39-40; 42pp; English.
 CC
 CC The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The
 CC present sequence is human MP-52 protein.
 XX
 SQ Sequence 120 AA;

Query Match 99.4%; Score 645; DB 22; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
 |||||||
 Db 2 PLATROGKRPSSKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61
 |||||||

QY 61 PTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
 |||||||
 Db 62 PTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120
 |||||||

RESULT 7
 ABG73290
 ID ABG73290 standard; Protein; 120 AA.
 XX
 AC ABG73290;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Amino acid sequence for human MP52.
 XX
 KW Human; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
 KW BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
 KW tendon/ligament-like tissue formation; trauma induced tendon defect;
 KW tendon/ligament-like tissue healing; tendon damage; ligament damage;
 KW tendon fixation; ligament fixation; congenital; ligament defect;
 KW cosmetic plastic surgery; vulnary; MP52.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Region 1..120
 FT /note= "Specifically claimed in Claim 26"
 FT Region 19..120
 FT /note= "Specifically claimed in Claim 26"
 XX
 PN US2002160494-A1.
 PD 31-OCT-2002.
 XX
 PF 31-AUG-2001; 2001US-0945182.
 XX
 PR 22-DEC-1994; 94US-0362670.
 PR 28-FEB-1997; 97US-0808324.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX
 PA (CELE/) CELESTE A J.
 PA (WOZN/) WOZNEY J M.
 PA (ROSE/) ROSEN V A.
 PA (WOLF/) WOLFMAN N M.
 PA (THOM/) THOMSEN G H.
 PA (MELT/) MELTON D A.
 XX
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 WPI; 2003-238228/23.
 DR N-PFDB; ABX11141.
 XX
 PT New bone morphogenetic proteins (designated BMP-12) or related
 PT proteins, useful for inducing tendon/ligament-like tissue formation in
 PT a patient, or for tendon/ligament-like tissue healing or repair (e.g.
 PT for treating tendonitis) -
 XX
 PS Claim 26; Page 21; 46pp; English.
 CC
 CC The present invention relates to the isolation of human bone
 CC morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein
 CC (designated BMP-13 or VL-1), and the polynucleotide sequences encoding

CC them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of
 CC proteins. BMP-12 and VL-1 are characterised by their ability to
 CC induce the formation of tendon/ligament-like tissue. The BMP-12
 CC proteins of the invention are useful for inducing tendon/ligament-like
 CC tissue formation in a patient. They are particularly useful for
 CC tendon/ligament-like tissue healing and tissue repair, e.g. for
 CC treating tendonitis, or other tendon or ligament defects in a patient.
 CC The polynucleotide sequences encoding the BMP-12 proteins are useful
 CC for inducing tendon/ligament-like tissue formation in a patient, and
 CC for tendon/ligament-like tissue healing and tissue repair. The BMP-12
 CC polypeptide and polynucleotide sequences may be used for preventing
 CC damage to tendon or ligament tissue, to improve fixation of tendon or
 CC ligament to bone or other tissues, to repair congenital or trauma
 CC induced tendon or ligament defects, and in cosmetic plastic surgery
 CC for attachment or repair of tendons or ligaments. The present sequence
 CC represents human MP52.
 XX
 SQ Sequence 120 AA;
 Query Match 99.4%; Score 645; DB 24; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKPSKRLKARCSKALHVNFKMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 60
 DB 2 PLATROGKPSKRLKARCSKALHVNFKMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 61
 QY 61 PTNHAIVQIILMSMDPEPTTACVPTRLSPISILFIDSANNVYKQYEDMVVSGCR 119
 DB 62 PTNHAIVQIILMSMDPEPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVSGCR 120
 RESULT 8
 AAR40800
 ID AAR40800 standard; Protein; 401 AA.
 XX
 AC AAR40800;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-FEB-1994 (first entry)
 XX
 DE TGF-beta-like clone MP-52 protein.
 XX
 KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
 KW bone; cartilage; tooth; wound repair; immunosuppressor;
 KW organ transplant; cosmetic surgery; antibody; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9316099-A2.
 XX
 PD 19-AUG-1993.
 XX
 PF 12-FEB-1993; 93WO-EP00350.
 XX
 PR 12-FEB-1992; 92EP-0102324.
 XX
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX
 PI Hoetten G, Neidhardt H;
 XX
 DR WPI; 1993-272824/34.
 DR N-PSDB; AAQ47709.
 XX
 PT New transforming growth factor-beta family proteins and DNA -
 PT used in tissue and wound repair, in treatment of bone, cartilage
 PT and tooth defects, and antibodies for diagnosis
 XX
 PS Claim 11; Page 19; 29pp; English.
 XX
 CC The sequences given in AAR40800 and AAR45447 represent fragments of
 CC embryo and liver derived human transforming growth factor-beta
 CC (TGF-beta) respectively. The full length protein may be used in a

CC pharmaceutical composition for the treatment of various bone, cartilage
 CC or tooth defects and in tissue and wound repair processes. These
 CC proteins may also be used as immunosuppressors in organ transplants and
 CC in cosmetic surgery. Antibodies raised against these proteins may be
 CC used for diagnostic purposes.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 401 AA;
 Query Match 99.4%; Score 645; DB 14; Length 401;
 Best Local Similarity 99.2%; Pred. No. 7.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKPSKRLKARCSKALHVNFKMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 60
 DB 283 PLATROGKPSKRLKARCSKALHVNFKMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 342
 QY 61 PTNHAIVQIILMSMDPEPTTACVPTRLSPISILFIDSANNVYKQYEDMVVSGCR 119
 DB 343 PTNHAIVQIILMSMDPEPTTCCVPTRLSPISILFIDSANNVYKQYEDMVVSGCR 401
 RESULT 9
 AAR69600
 ID AAR69600 standard; Protein; 501 AA.
 XX
 AC AAR69600;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-OCT-1995 (first entry)
 XX
 DE New TGF-beta family member - MP-52 protein sequence.
 XX
 KW Transforming growth factor-beta family; mitogenic; differentiation;
 KW treatment; prevention; disease; bone; cartilage; connective tissue;
 KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
 KW tissue regeneration; arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 382
 FT /label= mature protein
 XX
 PN WO9504819-A1.
 XX
 PD 16-FEB-1995.
 XX
 PF 09-AUG-1994; 94WO-EP03630.
 XX
 PR 10-AUG-1993; 93DE-4326829.
 PR 25-MAY-1994; 94DE-4418222.
 PR 09-JUN-1994; 94DE-4420157.
 XX
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX
 PI Hotten G, Neidhardt H, Paulista M, Hoetten G;
 XX
 DR WPI; 1995-090897/12.
 DR N-PSDB; AAQ83695.
 XX
 PT New DNA encoding a new member of the TGF beta family - and
 PT related vectors, host cells etc., has mitogenic and
 PT differentiation inducing activity, e.g. for treating or
 PT preventing diseases of bone and cartilage etc.
 XX
 PS Claim 6; Page 36; 51pp; German.
 XX
 CC The amino acid sequence of a novel member of the transforming growth
 CC factor-beta (TGF-b) family named MP-52. The gene encodes a protein
 CC of 501 amino acids (AA). The protein, or at least the mature protein,
 CC has mitogenic and/or differentiation inducing properties useful in
 CC the treatment or prevention of diseases of bone, cartilage, connective

CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
 CC be used for wound healing and tissue regeneration e.g. in osteoporosis
 CC and arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 501 AA;
 Query Match 99.4%; Score 645; DB 16; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
 DB 383 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 442
 QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 443 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501
 RESULT 10
 AAW36100
 ID AAW36100 standard; Protein; 501 AA.
 AC AAW36100;
 DT 08-MAY-1998 (first entry)
 XX Human MP52.
 DE
 KW Bone morphogenetic protein; BMP; processing enzyme; MP52;
 KW BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.
 OS Homo sapiens.
 XX
 PN WO9741250-AL.
 XX
 PD 06-NOV-1997.
 XX
 PF 28-APR-1997; 97WO-JP01474.
 XX
 PR 30-APR-1996; 96JP-0130618.
 XX
 PA (FARH) HOECHST YAKUHIN KOGYO KK.
 PA (FARH) HOECHST PHARM & CHEM KK.
 XX
 PI Kimura M, Makishima F, Takahashi M;
 DR WPT; 1997-549748/50.
 XX N-PSDB; AAT98191.
 XX
 PT Production of mature bone morphogenetic protein - by treatment of
 PT precursor protein with a processing enzyme such as furin either
 PT directly or by expressing them both in the same host
 XX
 PS Example 1; Pages 21-25; 34pp; Japanese.
 CC
 CC The present sequence is MP52, which is a bone morphogenetic
 CC protein (BMP).
 CC Mature BMP can be produced by directly adding a BMP processing
 CC enzyme to a solution containing BMP precursor protein, or by
 CC transforming an animal cell with expression vectors containing DNA
 CC encoding the enzyme and precursor protein, culturing the
 CC transformant and isolating the mature BMP from the culture. The
 CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,
 CC which can be used to treat bone formation or regeneration
 CC abnormalities.
 XX
 SQ Sequence 501 AA;
 Query Match 99.4%; Score 645; DB 18; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
 DB 383 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 442
 QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 443 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501
 RESULT 11
 AAW19210
 ID AAW19210 standard; Protein; 501 AA.
 AC AAW19210;
 DT 04-MAR-1998 (first entry)
 XX Human TGF-beta protein MP52.
 DE
 KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;
 KW cartilage; bone inducing activity; inhibit; bone resorption.
 XX
 OS Homo sapiens.
 PN DEL9548476-AL.
 XX
 PD 26-JUN-1997.
 XX
 PF 22-DEC-1995; 95DE-1048476.
 XX
 PR 22-DEC-1995; 95DE-1048476.
 XX
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX
 PI Bechtold R, Hotten G, Paulista M, Pohl J, Hoetten G;
 DR WPT; 1997-333931/31.
 XX N-PSDB; AAT69695.
 XX
 PT Compound containing protein from TGF-beta superfamily - has bone
 PT and/or cartilage inducing activity, useful in treatment of, e.g.
 PT osteoporosis, bone damage, Paget's disease and osteoarthritis
 XX
 PS Claim 3; Page 9; 10pp; German.
 CC
 CC This sequence is the human transforming growth factor (TGF)-beta protein
 CC designated MP52. MP52 can be used in a compound of formula (I):
 CC A-X(1-20)-B(1-20) (I); A = protein, or fragment, of the TGF-beta
 CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);
 CC B = 1 or more substituent groups with an affinity to the extracellular
 CC matrix, cellular components of bone and/or cartilage and/or to a
 CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer
 CC groups. The compound may be used to inhibit bone resorption, prevent or
 CC treat bone or cartilage related disorders, including osteoporosis,
 CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthritis and
 CC to treat bone or cartilage damage caused by wounding or overloading.
 XX
 SQ Sequence 501 AA;
 Query Match 99.4%; Score 645; DB 18; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
 DB 383 PLATROGKRPSKNLKARCSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEFFPLRSHLE 442
 QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 119
 DB 443 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGCR 501

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RESULT 12
AAW11900
ID AAW11900 standard; Protein; 501 AA.
XX
AC AAW11900;
XX
DT 28-OCT-1997 (first entry)
XX
DE Human high mol. wt. protein MP52, a growth/differentiation factor.
XX
KW Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW wound healing; regeneration; skeletal disorder; fracture; dimer.
XX
OS Homo sapiens.
XX
PN WO9704095-A1.
XX
PD 06-FEB-1997.
XX
PF 24-JUL-1996; 96WO-JP02065.
XX
PR 24-JUL-1995; 95JP-0218022.
XX
PA (FARH ) HOECHST JAPAN LTD.
PA (FARH ) HOECHST PHARM & CHEM KK.
PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
XX
DR WPI; 1997-132636/12.
DR N-PSDB; AAT61412.
XX
PT High molecular weight human MP52 growth or differentiation factor -
PT promotes bone induction, is useful for treatment and prevention of
PT bone disease
XX
PS Claim 1; Page 12-16; 25pp; Japanese.
XX
CC AAW11900 is a high mol. wt. form of a human growth/differentiation
CC factor MP52. MP52 promotes bone induction and is useful for plastic
CC reconstructive surgery, cosmetic facial treatment, bone transplantation
CC and tooth implantation. It is also useful for the treatment and
CC prevention of disorders of bone formation, bone, cartilage, joint
CC tissue, skin, mucous membranes, nails or teeth; for wound treatment and
CC tissue regeneration; and for the treatment of skeletal disorders and
CC fractures.
XX
SQ Sequence 501 AA;
Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
DT 1 1 PLATROGKRSKLNKARCSRKALHVNFKDGMWDWIIAPLEYEAPHCHGCEFFLRSHLE 60
DB 383 PLATROGKRSKLNKARCSRKALHVNFKDGMWDWIIAPLEYEAPHCHGCEFFLRSHLE 442
QY 61 PTNHAVIQTILMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIQTILMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 13
AAW01799
ID AAW01799 standard; Protein; 501 AA.
XX
AC AAW01799;
XX
DT 15-OCT-1997 (first entry)
XX
DE Human MP52 protein.
XX
KW Human; MP52; transforming growth factor; TGF; beta; medication;

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KW treatment; prevention; nervous system; disease; neuropathology;
KW ageing.
XX
OS Homo sapiens.
XX
PN DE19525416-A1.
XX
PD 16-JAN-1997.
XX
PF 12-JUL-1995; 95DE-1025416.
XX
PR 12-JUL-1995; 95DE-1025416.
XX
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
PI Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;
XX
DR WPI; 1997-078343/08.
DR N-PSDB; AAT59405.
XX
PT Medicaments contg. protein MP52 - useful for treating neurological
PT disorders
XX
PS Claim 2; Pages 12-14; 21pp; German.
XX
CC The present sequence is the human MP52 protein, which is
CC described in WO 9316099 and 9504819 as a member of the human
CC transforming growth factor beta superfamily. Active MP52 can be
CC used in a medicament to treat and prevent nervous system diseases,
CC and/or to treat neuropathological conditions caused by nervous
CC system ageing.
XX
SQ Sequence 501 AA;
Query Match 99.4%; Score 645; DB 18; Length 501;
Best Local Similarity 99.2%; Pred. No. 1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 PLATROGKRSKLNKARCSRKALHVNFKDGMWDWIIAPLEYEAPHCHGCEFFLRSHLE 60
DB 383 PLATROGKRSKLNKARCSRKALHVNFKDGMWDWIIAPLEYEAPHCHGCEFFLRSHLE 442
QY 61 PTNHAVIQTILMSMDPESTPTTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 443 PTNHAVIQTILMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 501

RESULT 14
AAW12770
ID AAW12770 standard; Protein; 501 AA.
XX
AC AAW12770;
XX
DT 11-MAY-1997 (first entry)
XX
DE Human bone morphogenic factor MP52 Arg.
XX
KW Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
KW connective tissue; mucous membrane; epithelium; teeth;
KW wound healing; vulnery; tissue regeneration; osteoporosis;
KW bone fracture; dental implant; osteoblast.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..27
FT Cleavage-site /label= sig_peptide
FT 380..381
FT /note= "sequencing suggests MP52 Arg is processed
FT proteolytically at Arg380-Arg381"
FT Cleavage-site 381..382
FT /note= "alternative cleavage site at Arg381-Ala382"
FT Mat_protein 381..501

```

FT /label= Mat.protein
 FT /note= "mature MP52 Arg preferred for use in
 FT compsns. of the invention"
 XX

PN W03706254-A1.

PD 20-FEB-1997.

XX 02-AUG-1996; 96WO-EP03427.

XX 03-AUG-1995; 95EP-0112241.

XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.

PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;

XX WPI; 1997-154261/14.

DR N-PSDB; AAT59729.

XX New human bone morphogenic factor, MP52 Arg - used in the treatment
 PT of osteoporosis and bone fracture, and for promoting bone regrowth

PS Claim 1; Page 12-15; 26pp; English.

XX Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
 CC factor that induces formation of cartilage from undifferentiated
 CC mesenchymal cells and which stimulates the differentiation and
 CC maturation of osteoblasts. It is effective for treating/preventing
 CC bone diseases caused by abnormal bone metabolism such as
 CC osteoporosis. It also accelerates the healing of bone fractures,
 CC and is useful for orthopaedic reconstruction, bone transplantation,
 CC and dental therapeutics because of its bone morphogenetic activity.
 CC It is also effective for preventing/treating cartilage, skin,
 CC connective tissue, mucous membrane, teeth and epithelial disorders.
 CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
 CC utilising an isolated DNA sequence (AAT59729) in plasmid pMS99.

XX Sequence 501 AA;

Query Match 99.4%; Score 645; DB 18; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKLNKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSLE 60

Db 383 PLATROGKRPSKLNKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSLE 442

QY 61 PTNHAIVQIPLMNSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

Db 443 PTNHAIVQIPLMNSMDPEPTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 15

AAW44868

ID AAW44868 standard; protein; 501 AA.

XX AC AAW44868;

DT 24-SEP-1998 (first entry)

XX TGF-beta superfamily subunit.

KW TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
 KW bone replacement; cartilage; bone; fracture.

XX Synthetic.

XX DE19647853-A1.

XX 20-MAY-1998.

XX 19-NOV-1996; 96DE-1047853.

XX

PR 19-NOV-1996; 96DE-1047853.
 XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 PA (GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.
 XX Heide H, Pabst J, Paulista M, Pohl J;
 PI WPI; 1998-287890/26.
 DR Bioactive Implant material for bone replacement - comprising
 XX osteogenic calcium phosphate matrix coated with protein
 PS Claim 3; Page 8-10; 12pp; German.

XX The TGF-beta superfamily subunit can be used together with a calcium
 CC phosphate matrix to produce a bioactive implant material for bone
 CC replacement. The implant has cartilage and/or bone-forming activity and
 CC can be used for local treatment of cartilage and/or bone diseases or
 CC damage caused by trauma, surgery, degeneration or overloading. The
 CC implant can also be used for the treatment of bone defects, e.g.
 CC parodontosis or fractures and in cosmetic and plastic surgery for fixing
 CC mobile bones.

XX Sequence 501 AA;

Query Match 99.4%; Score 645; DB 19; Length 501;
 Best Local Similarity 99.2%; Pred. No. 1e-58;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPSKLNKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSLE 60

Db 383 PLATROGKRPSKLNKARCSKALHVNFKDMGWDWIIAPLEYAFHCEGLCEFFPLRSLE 442

QY 61 PTNHAIVQIPLMNSMDPEPTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119

Db 443 PTNHAIVQIPLMNSMDPEPTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

Search completed: September 26, 2003, 17:56:44
 Job time : 86 secs

Db 2 PLATROGKRPKNLKARCSKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 61
QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
|||||
Db 62 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120
|||||
RESULT 2
US-08-333-576C-4
; Sequence 4, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald A.
; APPLICANT: Melton, Douglas H.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,576C
; FILING DATE: No. 6027919ember 2, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-333-576C-4
Query Match 99.4%; Score 645; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATROGKRPKNLKARCSKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
Db 2 PLATROGKRPKNLKARCSKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 61
QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
Db 62 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120
RESULT 3
US-08-808-324-4
; Sequence 4, Application US/08808324
; Patent No. 6284872
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil

; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,324
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-324-4
Query Match 99.4%; Score 645; DB 3; Length 120;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLATROGKRPKNLKARCSKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 60
Db 2 PLATROGKRPKNLKARCSKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFFPLRSHLE 61
QY 61 PTNHAVIOTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 119
Db 62 PTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 120
RESULT 4
PCT-US94-14030A-4
; Sequence 4, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14030A-4

Query Match 99.4%; Score 645; DB 5; Length 120;

Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKLNKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
|||||
Db 2 PLATQGRKPSKLNKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 61
|||||
Qy 61 PTHNAVIOFLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
|||||
Db 62 PTHNAVIOFLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 120
|||||

RESULT 5

US-08-289-222E-3
Sequence 3, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARCEL STEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 08/289,222E
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-3

Query Match 99.4%; Score 645; DB 3; Length 401;

Best Local Similarity 99.2%; Pred. No. 6.2e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATQGRKPSKLNKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 60
|||||
Db 283 PLATQGRKPSKLNKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEFFPLRSHLE 342
|||||
Qy 61 PTHNAVIOFLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
|||||
Db 343 PTHNAVIOFLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
|||||

RESULT 6

US-09-054-526B-3
Sequence 3, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H T TEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARCEL STEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/054,526B
FILING DATE: 08/289,222
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN

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;
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-8005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-054-526B-3

Query Match          99.4%; Score 645; DB 3; Length 401;
Best Local Similarity 99.2%; Pred. No. 6.2e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 60
   |||||||
Db 283 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 342
   |||||||

QY 61 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
   |||||||
Db 343 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 401
   |||||||

RESULT 7
US-08-288-508C-2
; Sequence 2, Application US/08288508C
; Patent No. 5994094
; GENERAL INFORMATION:
; APPLICANT: H tten, Gertrud
; APPLICANT: Neidhardt, Helge
; APPLICANT: Paulista, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
; TITLE OF INVENTION: THE TGF- FAMILY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentLin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,508C
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 26 829.3
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 18 222.8
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 20 157.5
; FILING DATE: 09-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: P-41,092
; REFERENCE/DOCKET NUMBER: P564-4019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-288-508C-2

Query Match          99.4%; Score 645; DB 2; Length 501;
Best Local Similarity 99.2%; Pred. No. 8.3e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 60
   |||||||
Db 383 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 442
   |||||||

QY 61 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
   |||||||
Db 443 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 501
   |||||||

RESULT 8
US-08-981-490B-1
; Sequence 1, Application US/08981490B
; Patent No. 6531450
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF
; TITLE OF INVENTION: NERVOUS SYSTEM
; FILE REFERENCE: 100564-07032
; CURRENT APPLICATION NUMBER: US/08/981,490B
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-981-490B-1

Query Match          99.4%; Score 645; DB 4; Length 501;
Best Local Similarity 99.2%; Pred. No. 8.3e-64;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 60
   |||||||
Db 383 PLATROGKRPKNLKCRCRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLE 442
   |||||||

QY 61 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 119
   |||||||
Db 443 PTNHAIVQITLMSMDPESTPTTCCVPTRLSPISILFIDSANNVVKQYEDMWVESCGR 501
   |||||||

RESULT 9
US-08-455-559-13
; Sequence 13, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
```

ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
US-08-455-559-13

Query Match 98.6%; Score 640; DB 1; Length 119;
Best Local Similarity 98.3%; Pred. No. 4.9e-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATQKRPKSNLKCARKSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSLE 60
DB 1 PLANQGRKRPKSNLKCARKSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSLE 60
QY 61 PTNHAIVQIILNMSDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 61 PTNHAIVQIILNMSDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119

RESULT 10
US-09-145-060-13
Sequence 13, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559

FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
US-09-145-060-13
Query Match 98.6%; Score 640; DB 3; Length 119;
Best Local Similarity 98.3%; Pred. No. 4.9e-64;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 PLATQKRPKSNLKCARKSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSLE 60
DB 1 PLANQGRKRPKSNLKCARKSRKALHVNFKDGMGDDWIIAPLEYEAFHCEGLCEPPLRSLE 60
QY 61 PTNHAIVQIILNMSDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
DB 61 PTNHAIVQIILNMSDPESTPTACVPTRLSPISILFIDSANNVVKQYEDMVVESCGR 119
RESULT 11
PCT-US94-00657-13
Sequence 13, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5


```
/
/
/ 2IP: 90067
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/00657
/ FILING DATE: 1/12/94
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WETHERELL, JR. PH.D., JOHN R.
/ REGISTRATION NUMBER: 31,678
/ REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619/455-5100
/ TELEFAX: 619-455-5110
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 495 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US94-00657-10

Query Match      98.6%; Score 640; DB 5; Length 495;
Best Local Similarity 98.3%; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROGKPSKLNKARSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLKSHLE 60
Db 377 PLANROGKPSKLNKARSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLKSHLE 436

QY 61 PTHAVITQILMSMDPESTPTACVPTPLSPISILFIDSANNVVKQYEDMWVESGCR 119
Db 437 PTHAVITQILMSMDPESTPTCCVPTPLSPISILFIDSANNVVKQYEDMWVESGCR 495

RESULT 15
US-08-335-583C-51
; Sequence 51, Application US/08335583C
; Patent No. 5693779
; GENERAL INFORMATION:
; APPLICANT: Moos Jr., Malcolm
; APPLICANT: Wang, Shouwan
; APPLICANT: Krinks, Marie
; TITLE OF INVENTION: PRODUCTION AND USE OF
; TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335.583C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH104.001A
; TELECOMMUNICATION INFORMATION:
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/
/
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 102 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: C-terminal
/ ORIGINAL SOURCE:
/ US-08-335-583C-51

Query Match      86.1%; Score 559; DB 1; Length 102;
Best Local Similarity 99.0%; Pred. No. 4.3e-55;
Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLEPTNHAVITQILMSMDPE 77
Db 1 CSRKALHVNFKDMGWDWIIAPLEYAFHCEGLCEPPLRSHLEPTNHAVITQILMSMDPE 60

QY 78 STEPTACVPTPLSPISILFIDSANNVVKQYEDMWVESGCR 119
Db 61 STEPTCCVPTPLSPISILFIDSANNVVKQYEDMWVESGCR 102

Search completed: September 26, 2003, 18:00:22
Job time : 30 secs
```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 26, 2003, 17:53:49 ; Search time 40 seconds
(without alignments)
286.102 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATQGRPSKNLKARCSR.....ANNVYKQYEDMVVESCGR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	99.4	501	2 JC2347	growth/differentiation
2	640	98.6	495	2 S43294	bone morphogenetic
3	639	98.5	501	2 A5452	cartilage-derived
4	543	83.7	125	2 S43295	bone morphogenetic
5	528	81.4	436	2 B5452	cartilage-derived
6	493	76.0	151	2 S43296	bone morphogenetic
7	353.5	54.5	461	2 S52408	SPDVR1 protein - s
8	347	53.5	393	2 S37073	bone morphogenetic
9	347	53.5	394	2 S45355	bone morphogenetic
10	347	53.5	396	1 BMH02	bone morphogenetic
11	347	53.5	401	2 JH0689	bone morphogenetic
12	346	53.3	400	2 A49147	bone morphogenetic
13	346	53.3	405	2 I50608	bone morphogenetic
14	344	53.0	588	2 A26158	decapentaplegic pr
15	343	52.9	398	2 JH0688	bone morphogenetic
16	343	52.9	398	2 JH0687	bone morphogenetic
17	341	52.5	408	2 S38343	bone morphogenetic
18	341	52.5	420	2 I49541	bone morphogenetic
19	339	52.2	408	1 BMH04	bone morphogenetic
20	338	52.1	408	2 S58791	bone morphogenetic
21	337	51.9	353	2 I50607	bone morphogenetic
22	333	51.3	207	2 S37618	vgr protein - rat
23	333	51.3	452	2 I49542	bone morphogenetic
24	333	51.3	454	1 BMH05	bone morphogenetic
25	332	51.2	513	1 BMH06	bone morphogenetic
26	331	51.0	408	2 JH0801	bone morphogenetic
27	330	50.8	313	2 I51284	bone morphogenetic
28	330	50.8	431	1 BMH07	bone morphogenetic
29	329	50.7	510	2 A54798	Vg-1-related prote

30 328 50.5 426 2 JH0690 bone morphogenetic
31 327 50.4 430 2 J01184 osteogenic protein
32 317.5 48.9 402 2 A45056 osteogenic protein
33 313 48.2 360 2 A29619 Vg1 embryonic grow
34 306.5 47.2 365 2 T43286 cet-1 protein - Ca
35 304 46.8 455 2 A43918 TGF-beta-related p
36 303 46.7 427 2 A40735 TGF beta homolog d
37 283.5 43.7 366 2 A46607 growth/differentia
38 281 43.3 472 1 BMH03 bone morphogenetic
39 279.5 43.1 360 2 I53032 bone morphogenetic
40 278.5 42.9 366 2 A45402 transforming growt
41 274 42.2 366 2 T03907 TGF-beta-related p
42 271.5 41.8 372 2 C39364 GDF-1 embryonic gr
43 268.5 41.4 476 2 JC4646 bone morphogenetic
44 264.5 40.8 357 2 A39364 GDF-1 embryonic gr
45 264.5 40.8 478 2 JC4838 bone morphogenetic

ALIGNMENTS

RESULT 1

JC2347

growth/differentiation factor 5 - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000

C:Accession: JC2347

R:Roetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.

Biochem. Biophys. Res. Commun. 204, 646-652, 1994

A>Title: Cloning and expression of recombinant human growth/differentiation factor 5
A:Reference number: JC2347; MUID:95071375; PMID:7980526

A:Accession: JC2347

A:Molecule type: DNA

A:Residues: 1-501 <HOE>

A:Cross-references: GB:X80915; NID:9671524; PIDN:CAA56874.1; PID:9671525

C:Genetics:

A:Gene: GDB:BMP9

A:Cross-references: GDB:433948

A:Introns: 211/1

C:Superfamily: inhibin

C:Keywords: glycoprotein

F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 99.4%; Score 645; DB 2; Length 501;
Best local similarity 99.2%; Pred. No. 4.6e-59;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATQGRPSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEPLRSHLE 60
|||||
Db 383 PLATQGRPSKNLKARCSRKALHVNFKDGMWDWIIAPLEYAFHCEGLCEPLRSHLE 442

QY 61 PTNHAVIQTLNMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
|||||

Db 443 PTNHAVIQTLNMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501
|||||

RESULT 2

S43294

bone morphogenetic protein-related protein (GDF5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000

C:Accession: S43294

R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.

Nature 368, 639-643, 1994

A>Title: Limb alterations in brachypodism mice due to mutations in a new member of t

A:Reference number: S43294; MUID:94195427; PMID:8143850

A:Accession: S43294

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-495 <STO>

A:Cross-references: GB:U08337; NID:g488461; PIDN:AAA18778.1; PID:g488462

C:Superfamily: inhibin

C:Accession: S52408
R:Ponce, M.R.; Nicol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A:Description: SPDR1, a member of the transforming growth factor-beta superfamily expressed in rat osteoblasts
A:Reference number: S52408
A:Accession: S52408
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <PDB>
A:Cross-references: EMBL:248313; NID:g673496; PID:g673497
C:Superfamily: inhibin

Query Match 54.5%; Score 353.5; DB 2; Length 461;
Best Local Similarity 48.1%; Pred. No. 7.3e-29;
Matches 65; Conservative 19; Mismatches 32; Indels 19; Gaps 2;

QY 3 ATRQ---GKPSK-----NLKARSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEPPLRSHLEPTN 43
DB 326 ATRQKQKRLKSKCKRHPLVDFSDVGNWDWIVAPPGYHAFYCHGECPPPLADHLNSTN 385
QY 44 APHCEGLCEPPLRSHLEPTNHAIVQTLNMSNDPESTPTACVPTLSPISILFIDSANNV 103
DB 386 AFTQCEGCAFFLNGHANTNHAIVQTLVHMSPSHVPOCCAPKLSPTLVLYDDSRNV 445
QY 104 VYQYEDMVVSCGC 118
DB 446 VLKYYKMYVRACGC 460

RESULT 8
S37073
bone morphogenetic protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
A:Accession: S37073
submitted to the EMBL Data Library, September 1993
A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein
A:Reference number: S37073
A:Accession: S37073
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <FEN>
A:Cross-references: EMBL:225868; NID:g397950; PIDN:CAA81088.1; PID:g397951
C:Superfamily: inhibin

Query Match 53.5%; Score 347; DB 2; Length 393;
Best Local Similarity 54.3%; Pred. No. 2.9e-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKRLKARSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEPPLRSHLEPTN 63
DB 279 RQAKHKQKRLKSKCKRHPLVDFSDVGNWDWIVAPPGYHAFYCHGECPPPLADHLNSTN 338
QY 64 HAVIQTLNMSNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 339 HAVIQTLNMSNVN-SKIPKACCVPTLSAISMILYLDENEKVKLVKNYQDMVVEGCGCR 393

RESULT 9
S45355
bone morphogenetic protein-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
A:Accession: S45355
R:Peng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Peng, M.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1218, 221-224, 1994
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comparison with human BMP-2
A:Reference number: S45355; MUID:94289485; PMID:8016727
A:Accession: S45355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <FEN>

C:Superfamily: inhibin

Query Match 53.5%; Score 347; DB 2; Length 394;
Best Local Similarity 54.3%; Pred. No. 2.9e-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKRLKARSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEPPLRSHLEPTN 63
DB 280 RQAKHKQKRLKSKCKRHPLVDFSDVGNWDWIVAPPGYHAFYCHGECPPPLADHLNSTN 339
QY 64 HAVIQTLNMSNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 340 HAVIQTLNMSNVN-SKIPKACCVPTLSAISMILYLDENEKVKLVKNYQDMVVEGCGCR 394

RESULT 10
BMH02
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2A; rhBMP2
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
A:Accession: B37278; PC2178
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 <WO2>
A:Cross-references: GB:M22489; NID:gi179501; PIDN:AAA51834.1; PID:gi179502
R:Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Ka J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in si cells
A:Reference number: PC2178; MUID:94266754; PMID:8208877
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 'X', 297-304 <ISH>
A:Experimental source: cell line BOMO-15A1C
R:Rathore, S.; Hammerstone, K.M.; Dausereau, S.; Porter, T.J. Protein Sci. 4(Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2) are biologically active
A:Reference number: A56729
A:Contents: annotation
A:Note: determination of amino ends of mature forms; dimers with long form chains have been observed
A:Comment: This hormone is capable of inducing bone formation at ectopic morphologic sites
C:Genetics:
A:Gene: GDB:BMP2; BMP2A
A:Cross-references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
C:Complex: homodimer, disulfide linked
C:Superfamily: inhibin
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-26/Domain: propeptide #status predicted <PRO>
F:266-396/Product: bone morphogenetic protein 2, long form #status predicted <MAT>
F:283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>
F:135,163,164,200/Binding site: carboxylic acid (Gln) (in mature form) #status predicted
F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expected
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental

C:Superfamily: inhibin

Query Match 53.5%; Score 347; DB 2; Length 394;
Best Local Similarity 54.3%; Pred. No. 2.9e-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKRLKARSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEPPLRSHLEPTN 63
DB 280 RQAKHKQKRLKSKCKRHPLVDFSDVGNWDWIVAPPGYHAFYCHGECPPPLADHLNSTN 339
QY 64 HAVIQTLNMSNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 340 HAVIQTLNMSNVN-SKIPKACCVPTLSAISMILYLDENEKVKLVKNYQDMVVEGCGCR 394

RESULT 10
BMH02
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2A; rhBMP2
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
A:Accession: B37278; PC2178
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 <WO2>
A:Cross-references: GB:M22489; NID:gi179501; PIDN:AAA51834.1; PID:gi179502
R:Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Ka J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in si cells
A:Reference number: PC2178; MUID:94266754; PMID:8208877
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 'X', 297-304 <ISH>
A:Experimental source: cell line BOMO-15A1C
R:Rathore, S.; Hammerstone, K.M.; Dausereau, S.; Porter, T.J. Protein Sci. 4(Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2) are biologically active
A:Reference number: A56729
A:Contents: annotation
A:Note: determination of amino ends of mature forms; dimers with long form chains have been observed
A:Comment: This hormone is capable of inducing bone formation at ectopic morphologic sites
C:Genetics:
A:Gene: GDB:BMP2; BMP2A
A:Cross-references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
C:Complex: homodimer, disulfide linked
C:Superfamily: inhibin
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-26/Domain: propeptide #status predicted <PRO>
F:266-396/Product: bone morphogenetic protein 2, long form #status predicted <MAT>
F:283-396/Product: bone morphogenetic protein 2 #status predicted <MAT>
F:135,163,164,200/Binding site: carboxylic acid (Gln) (in mature form) #status predicted
F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expected
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 53.5%; Score 347; DB 1; Length 396;
Best Local Similarity 54.3%; Pred. No. 2.9e-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQK-RPSKRLKARSKALHVNFKMGWDDWIIAPLEYAFHCEGLCEPPLRSHLEPTN 63
DB 282 RQAKHKQKRLKSKCKRHPLVDFSDVGNWDWIVAPPGYHAFYCHGECPPPLADHLNSTN 341
QY 64 HAVIQTLNMSNDPESTPTACVPTLSPISILFIDSANNVYKQYEDMVVSCGCR 119
DB 342 HAVIQTLNMSNVN-SKIPKACCVPTLSAISMILYLDENEKVKLVKNYQDMVVEGCGCR 396

```
RESULT 11
JH0689
bone morphogenetic protein 4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0689
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A:Reference number: JH0687; MUID:92378616; PMID:1510675
A:Accession: JH0689
A:Molecule type: mRNA
A:Residues: 1-401 <NLS>
A:Cross-references: GB:X63426; NID:g64587; PIDN:CAA45020.1; PID:g64588
A:Experimental source: oocyte
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:288-401/Product: bone morphogenetic protein 4 #status predicted <MAT>
F:141,204,238,343,358/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.5%; Score 347; DB 2; Length 401;
Best Local Similarity 52.1%; Pred. No. 3e-28;
Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TROGKPSKNLAKR-----CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSH 58
DB 282 TRSKRSPKQPRKKNKCHRRSLYVDFSDVGNWNIIVAPPGYQAFYCHGDCPPLADH 341

QY 59 LEPTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVYVSGCG 118
DB 342 LNSTNHAIVQTLVNSVN-SSIPKACCVPTLSAISMLYLDYDKVLYKNQYEMVYVSGCG 400

QY 119 R 119
DB 401 R 401

RESULT 12
A49147
bone morphogenetic protein 4 - African clawed frog
N:Alternate names: BMP-4; ventralizing factor
C:Species: Xenopus laevis (African clawed frog)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A49147
R:Dale, L.; Howes, G.; Price, B.M.; Smith, J.C.
Development 115, 573-585, 1992
A:Title: Bone morphogenetic protein 4: a ventralizing factor in early Xenopus developmen
A:Reference number: A49147; MUID:93048819; PMID:1425340
A:Accession: A49147
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-400 <DAL>
A:Cross-references: GB:X64538; GB:S46999; NID:g64589; PIDN:CAA45836.1; PID:g64590
A:Experimental source: XTC cells
A:Note: sequence extracted from NCBI backbone (NCBIN:117127, NCBIPI:117128)
C:Superfamily: inhibin

Query Match 53.3%; Score 346; DB 2; Length 400;
Best Local Similarity 52.1%; Pred. No. 3.8e-28;
Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TROGKPSKNLAKR-----CSRKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSH 58
DB 281 TRSKRSPKQPRKKNKCHRRSLYVDFSDVGNWNIIVAPPGYQAFYCHGDCPPLADH 340

QY 59 LEPTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVYVSGCG 118
DB 341 LNSTNHAIVQTLVNSVN-ASIPKACCVPTLSAISMLYLDYDKVLYKNQYEMVYVSGCG 399

QY 119 R 119
DB 400 R 400
```

```
RESULT 13
I50608
bone morphogenetic protein 4 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I50608
R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
Development 120, 209-218, 1994
A:Title: Bone morphogenetic proteins and a signalling pathway that controls patternit
A:Reference number: I50607; MUID:94163974; PMID:8119128
A:Accession: I50608
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-405 <FRA>
A:Cross-references: EMBL:X75915; NID:g472929; PIDN:CAA53514.1; PID:g472930
C:Genetics:
C:Superfamily: inhibin

Query Match 53.3%; Score 346; DB 2; Length 405;
Best Local Similarity 52.1%; Pred. No. 3.8e-28;
Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;

QY 4 TROGKRP-----SKNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSH 58
DB 286 FRARRSPKHGSRKKNKCHRRSLYVDFSDVGNWNIIVAPPGYQAFYCHGDCPPLADH 345

QY 59 LEPTNHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVYVSGCG 118
DB 346 LNSTNHAIVQTLVNSVN-SSIPKACCVPTLSAISMLYLDYDKVLYKNQYEMVYVSGCG 404

QY 119 R 119
DB 405 R 405

RESULT 14
A26158
decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
C:Accession: A26158
R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
Nature 325, 81-84, 1987
A:Title: A transcript from a Drosophila pattern gene predicts a protein homologous to
A:Reference number: A26158; MUID:87090408; PMID:3467201
A:Accession: A26158
A:Molecule type: mRNA
A:Residues: 1-588 <PAD>
A:Cross-references: GB:M30116; NID:gl57291; PID:gl57292
C:Genetics:
A:Gene: FlyBase:dpp
A:Cross-references: FlyBase:FBgn0000490
C:Keywords: glycoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.0%; Score 344; DB 2; Length 588;
Best Local Similarity 48.7%; Pred. No. 9.3e-28;
Matches 57; Conservative 24; Mismatches 34; Indels 2; Gaps 1;

QY 5 ROGKPPS--KNLKARCSKALHVNFKDMGWDWIIAPLEYEAFHCEGLCEPPLRSHLEPT 62
DB 472 RRARPTRKNDTCRRSLYVDFSDVGNWNIIVAPPGYQAFYCHGDCPPLADHFNST 531

QY 63 NHAVIQTLMNSMDPESTPTACVPTRLSPISILFIDSANNVYKQYEDMVYVSGCGR 119
DB 532 NHAVVQTLVNNMFPKVPKACCVPTQLDSVAMLYLNDQSTVYLKNQYEMVYVSGCGR 588

RESULT 15
JH0688
```

bone morphogenetic protein 2II precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0688
 R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
 A:Reference number: JH0687; MUID:92378616; PMID:1510675
 A:Accession: JH0688
 A:Molecule type: mRNA
 A:Residues: 1-398 <NIS>
 A:Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
 A:Experimental source: oocyte
 C:Superfamily: inhibitor
 C:Keywords: glycoprotein
 F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
 F:137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.9%; Score 343; DB 2; Length 398;
 Best local similarity 53.4%, Pred. No. 7.6e-28;
 Matches 62; Conservative 19; Mismatches 33; Indels 2; Gaps 2;
 QY 5 RQK-RPSKRLKARSKALHVNFKDWDWIIAPLEYEAFHCEGLCEPFLKSHLEPTN 63
 || : | ||: | : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
 Db 284 RQARHKQRKRLKSSCRHPLYVDVDSVGNWDMIVAPPGYHAFYCHGCEPPLADHLNSTN 343
 ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
 QY 64 HAVIQTLNMSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 119
 ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
 Db 344 HAIYQTLNVSNN-TNIPKACCVPTLSTLSMLYLDENEKVVLYKNYQDMVYVESCGR 398

Search completed: September 26, 2003, 17:59:45
 Job time : 40 secs